

SEQUENCE LISTING

<110> Duvick, Jonathan P.
Gilliam, Jacob T.
Maddox, Joyce R.
Rao, Aragula Gururaj
Crasta, Oswald R.
Folkerts, Otto

<120> Amino Polyol Amine Oxidase
Polynucleotides and Related Polypeptides and Methods of Use

<130> 1134R

<150> US 60/092,936

<151> 1998-07-25

<150> US 60/135,391

<151> 1999-05-21

<150> US 09/352,159

<151> 1999-07-12

<150> US 09/352,168

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<160> 53

<170> FastSEQ for Windows Version 3.0

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<213> *Exophiala spinifera*

<220>

<221> misc_feature

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attgtcgatc	gacgtcgatg	ctggatatctc	tggcaaatga	gatgggggtca	cagctcgatt	180
ggaggacgcc	cgagaagcct	tgttcgcgcc	accacggctt	gtcccatacg	aagactatct	240
tgctatagta	gcccaggata	gaattttccg	ccaatgcttg	cttctcggcg	ggaagagggtg	300
gtgaaaatgt	caaggtggga	tacaaggttg	tcggtaacga	aaccancacc	tttttgcttc	360
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<213> *Exophiala spinifera*

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gatcgtactg	tacagccgga	tgccgactgc	tcaatttcag	cgacgggggt	gttgagggtgc	180
ac						182

<210> 3
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Designed oligonucleotide for 3' RACE, N21965

<400> 3
 tgggtttcgtt accgacaacc ttgtatccc 29

<210> 4
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<220>
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<400> 4
 gagttggtcc cagacagact tttgtcgt 28

<210> 5
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<220>
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 Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly Leu
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gag acg gca cgc aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt ctt 96
 Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu
 20 25 30

gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tcc ggt 144
 Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly
 35 40 45

ccc ggc agg acg act atc aac gac ctc ggc gct gcg tgg atc aat gac 192
 Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp
 50 55 60

agc aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg gag 240
 Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu
 65 70 75 80

ggc gag ctc cag agg acg act gga aat tca atc cat caa gca caa gac 288
 Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp
 85 90 95

ggt aca acc act aca gct cct tat ggt gac tcc ttg ctg agc gag gag 336
 Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu
 100 105 110

gtt gca agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg atc 384

Val	Ala	Ser	Ala	Leu	Ala	Glu	Leu	Leu	Pro	Val	Trp	Ser	Gln	Leu	Ile		
		115					120					125					
gaa	gag	cat	agc	ctt	caa	gac	ctc	aag	gcg	agc	cct	cag	gcg	aag	cgg		432
Glu	Glu	His	Ser	Leu	Gln	Asp	Leu	Lys	Ala	Ser	Pro	Gln	Ala	Lys	Arg		
		130				135					140						
ctc	gac	agt	gtg	agc	ttc	gcg	cac	tac	tgt	gag	aag	gaa	cta	aac	ttg		480
Leu	Asp	Ser	Val	Ser	Phe	Ala	His	Tyr	Cys	Glu	Lys	Glu	Leu	Asn	Leu		
					150					155					160		
cct	gct	gtt	ctc	ggc	gta	gca	aac	cag	atc	aca	cgc	gct	ctg	ctc	ggt		528
Pro	Ala	Val	Leu	Gly	Val	Ala	Asn	Gln	Ile	Thr	Arg	Ala	Leu	Leu	Gly		
				165				170						175			
gtg	gaa	gcc	cac	gag	atc	agc	atg	ctt	ttt	ctc	acc	gac	tac	atc	aag		576
Val	Glu	Ala	His	Glu	Ile	Ser	Met	Leu	Phe	Leu	Thr	Asp	Tyr	Ile	Lys		
			180					185					190				
agt	gcc	acc	ggt	ctc	agt	aat	att	ttc	tcg	gac	aag	aaa	gac	ggc	ggg		624
Ser	Ala	Thr	Gly	Leu	Ser	Asn	Ile	Phe	Ser	Asp	Lys	Lys	Asp	Gly	Gly		
		195					200					205					
cag	tat	atg	cga	tgc	aaa	aca	ggt	atg	cag	tcg	att	tgc	cat	gcc	atg		672
Gln	Tyr	Met	Arg	Cys	Lys	Thr	Gly	Met	Gln	Ser	Ile	Cys	His	Ala	Met		
		210				215					220						
tca	aag	gaa	ctt	gtt	cca	ggc	tca	gtg	cac	ctc	aac	acc	ccc	gtc	gct		720
Ser	Lys	Glu	Leu	Val	Pro	Gly	Ser	Val	His	Leu	Asn	Thr	Pro	Val	Ala		
		225			230					235				240			
gaa	att	gag	cag	tcg	gca	tcc	ggc	tgt	aca	gta	cga	tcg	gcc	tcg	ggc		768
Glu	Ile	Glu	Gln	Ser	Ala	Ser	Gly	Cys	Thr	Val	Arg	Ser	Ala	Ser	Gly		
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gcc	gtg	ttc	cga	agc	aaa	aag	gtg	gtg	gtt	tcg	tta	ccg	aca	acc	ttg		816
Ala	Val	Phe	Arg	Ser	Lys	Lys	Val	Val	Val	Ser	Leu	Pro	Thr	Thr	Leu		
			260					265					270				
tat	ccc	acc	ttg	aca	ttt	tca	cca	cct	ctt	ccc	gcc	gag	aag	caa	gca		864
Tyr	Pro	Thr	Leu	Thr	Phe	Ser	Pro	Pro	Leu	Pro	Ala	Glu	Lys	Gln	Ala		
		275					280					285					
ttg	gcg	gaa	aat	tct	atc	ctg	ggc	tac	tat	agc	aag	ata	gtc	ttc	gta		912
Leu	Ala	Glu	Asn	Ser	Ile	Leu	Gly	Tyr	Tyr	Ser	Lys	Ile	Val	Phe	Val		
		290				295					300						
tgg	gac	aag	ccg	tgg	tgg	cgc	gaa	caa	ggc	ttc	tcg	ggc	gtc	ctc	caa		960
Trp	Asp	Lys	Pro	Trp	Trp	Arg	Glu	Gln	Gly	Phe	Ser	Gly	Val	Leu	Gln		
		305			310				315					320			
tcg	agc	tgt	gac	ccc	atc	tca	ttt	gcc	aga	gat	acc	agc	atc	gac	gtc		1008
Ser	Ser	Cys	Asp	Pro	Ile	Ser	Phe	Ala	Arg	Asp	Thr	Ser	Ile	Asp	Val		
				325				330						335			
gat	cga	caa	tgg	tcc	att	acc	tgt	ttc	atg	gtc	gga	gac	ccg	gga	cgg		1056
Asp	Arg	Gln	Trp	Ser	Ile	Thr	Cys	Phe	Met	Val	Gly	Asp	Pro	Gly	Arg		
			340				345					350					
aag	tgg	tcc	caa	cag	tcc	aag	cag	gta	cga	caa	aag	tct	gtc	tgg	gac		1104
Lys	Trp	Ser	Gln	Gln	Ser	Lys	Gln	Val	Arg	Gln	Lys	Ser	Val	Trp	Asp		
		355					360					365					

caa ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag ccg	1152
Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro	
370 375 380	
gcc aac gtg ctc gaa atc gag tgg tcg aag cag cag tat ttc caa gga	1200
Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly	
385 390 395 400	
gct ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt tcg	1248
Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser	
405 410 415	
gcg ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag acg	1296
Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr	
420 425 430	
tct tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tcg ggt caa	1344
Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln	
435 440 445	
cga ggt gct gca gaa gtt gtg gct agc ctg gtg cca gca gca	1386
Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala	
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tag	1389

<210> 6
 <211> 462
 <212> PRT
 <213> Exophiala spinifera

<400> 6

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		20						25				30			
Glu	Ala	Met	Asp	Arg	Val	Gly	Gly	Lys	Thr	Leu	Ser	Val	Gln	Ser	Gly
		35					40					45			
Pro	Gly	Arg	Thr	Thr	Ile	Asn	Asp	Leu	Gly	Ala	Ala	Trp	Ile	Asn	Asp
	50					55					60				
Ser	Asn	Gln	Ser	Glu	Val	Ser	Arg	Leu	Phe	Glu	Arg	Phe	His	Leu	Glu
65					70					75				80	
Gly	Glu	Leu	Gln	Arg	Thr	Thr	Gly	Asn	Ser	Ile	His	Gln	Ala	Gln	Asp
			85					90						95	
Gly	Thr	Thr	Thr	Thr	Ala	Pro	Tyr	Gly	Asp	Ser	Leu	Leu	Ser	Glu	Glu
			100					105						110	
Val	Ala	Ser	Ala	Leu	Ala	Glu	Leu	Leu	Pro	Val	Trp	Ser	Gln	Leu	Ile
		115					120					125			
Glu	Glu	His	Ser	Leu	Gln	Asp	Leu	Lys	Ala	Ser	Pro	Gln	Ala	Lys	Arg
	130					135					140				
Leu	Asp	Ser	Val	Ser	Phe	Ala	His	Tyr	Cys	Glu	Lys	Glu	Leu	Asn	Leu
145					150					155				160	
Pro	Ala	Val	Leu	Gly	Val	Ala	Asn	Gln	Ile	Thr	Arg	Ala	Leu	Leu	Gly
			165					170						175	
Val	Glu	Ala	His	Glu	Ile	Ser	Met	Leu	Phe	Leu	Thr	Asp	Tyr	Ile	Lys
		180					185						190		
Ser	Ala	Thr	Gly	Leu	Ser	Asn	Ile	Phe	Ser	Asp	Lys	Lys	Asp	Gly	Gly
	195					200						205			
Gln	Tyr	Met	Arg	Cys	Lys	Thr	Gly	Met	Gln	Ser	Ile	Cys	His	Ala	Met
	210					215					220				
Ser	Lys	Glu	Leu	Val	Pro	Gly	Ser	Val	His	Leu	Asn	Thr	Pro	Val	Ala

225		230		235		240
Glu Ile Glu Gln Ser	Ala Ser Gly Cys Thr	Val Arg Ser Ala Ser	Gly			
	245		250		255	
Ala Val Phe Arg Ser	Lys Lys Val Val	Val Ser Leu Pro Thr	Thr Leu			
	260		265		270	
Tyr Pro Thr Leu Thr	Phe Ser Pro Pro	Leu Pro Ala Glu Lys	Gln Ala			
	275		280		285	
Leu Ala Glu Asn Ser	Ile Leu Gly Tyr Tyr	Ser Lys Ile Val Phe	Val			
	290		295		300	
Trp Asp Lys Pro Trp	Trp Arg Glu Gln Gly	Phe Ser Gly Val Leu	Gln			
305		310		315		320
Ser Ser Cys Asp Pro	Ile Ser Phe Ala Arg	Asp Thr Ser Ile Asp	Val			
	325		330		335	
Asp Arg Gln Trp Ser	Ile Thr Cys Phe Met	Val Gly Asp Pro Gly	Arg			
	340		345		350	
Lys Trp Ser Gln Gln	Ser Lys Gln Val Arg	Gln Lys Ser Val Trp	Asp			
	355		360		365	
Gln Leu Arg Ala Ala	Tyr Glu Asn Ala Gly	Ala Gln Val Pro Glu	Pro			
	370		375		380	
Ala Asn Val Leu Glu	Ile Glu Trp Ser Lys	Gln Gln Tyr Phe Gln	Gly			
385		390		395		400
Ala Pro Ser Ala Val	Tyr Gly Leu Asn Asp	Leu Ile Thr Leu Gly	Ser			
	405		410		415	
Ala Leu Arg Thr Pro	Phe Lys Ser Val His	Phe Val Gly Thr Glu	Thr			
	420		425		430	
Ser Leu Val Trp Lys	Gly Tyr Met Glu Gly	Ala Ile Arg Ser Gly	Gln			
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Arg Gly Ala Ala Glu	Val Val Ala Ser Leu	Val Pro Ala Ala				
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<210> 7
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 <213> *Exophiala spinifera*

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 <222> (1) ... (646)

 <221> intron
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1 5 10 15																		
gag acg gca cgc aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt ctt																		96
Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu																		
20 25 30																		
gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tgc ggt																		144
Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly																		
35 40 45																		
ccc ggc agg acg act atc aac gac ctc ggc gct gcg tgg atc aat gac																		192
Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp																		
50 55 60																		

agc aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg gag	240
Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu	
65 70 75 80	
ggc gag ctc cag agg acg act gga aat tca atc cat caa gca caa gac	288
Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp	
85 90 95	
ggt aca acc act aca gct cct tat ggt gac tcc ttg ctg agc gag gag	336
Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu	
100 105 110	
gtt gca agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg atc	384
Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile	
115 120 125	
gaa gag cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag cgg	432
Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg	
130 135 140	
ctc gac agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac ttg	480
Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu	
145 150 155 160	
cct gct gtt ctc ggc gta gca aac cag atc aca cgc gct ctg ctc ggt	528
Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly	
165 170 175	
gtg gaa gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc aag	576
Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys	
180 185 190	
agt gcc acc ggt ctc agt aat att ttc tcg gac aag aaa gac ggc ggg	624
Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly	
195 200 205	
cag tat gtg cga tgc aaa aca g gtgcgtgtgg tgtcgtctca ggtgggggac	676
Gln Tyr Val Arg Cys Lys Thr	
210 215	
tcgtttctca gtggtcattc cag gt atg cag tcg att tgc cat gcc atg tca	728
Gly Met Gln Ser Ile Cys His Ala Met Ser	
220 225	
aag gaa ctt gtt cca ggc tca gtg cac ctc aac acc ccc gtc gct gaa	776
Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala Glu	
230 235 240	
att gag cag tcg gca tcc ggc tgt aca gta cga tcg gcc tcg ggc gcc	824
Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala	
245 250 255	
gtg ttc cga agc aaa aag gtg gtg gtt tcg tta ccg aca acc ttg tat	872
Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr	
260 265 270	
ccc acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa gca ttg	920
Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu	
275 280 285	
gcg gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc gta tgg	968
Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp	

290	295	300	305	
gac aag ccg tgg tgg cgc gaa caa ggc ttc tcg ggc gtc ctc caa tcg				1016
Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser	310	315	320	
agc tgt gac ccc atc tca ttt gcc aga gat acc agc atc gac gtc gat				1064
Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp	325	330	335	
cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga cgg aag				1112
Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys	340	345	350	
tgg tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg gac caa				1160
Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln	355	360	365	
ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag ccg gcc				1208
Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala	370	375	380	385
aac gtg ctc gaa atc gag tgg tcg aag cag cag tat ttc caa gga gct				1256
Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala	390	395	400	
ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt tcg gcg				1304
Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala	405	410	415	
ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag acg tct				1352
Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr Ser	420	425	430	
tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tcg ggt caa cga				1400
Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg	435	440	445	
ggg gct gca gaa gtt gtg gct agc ctg gtg cca gca gca tag				1442
Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala	450	455	460	

<210> 8
 <211> 462
 <212> PRT
 <213> *Exophiala spinifera*

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 Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly
 35 40 45
 Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp
 50 55 60
 Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu
 65 70 75 80
 Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp
 85 90 95
 Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu

Val	Ala	Ser	100	Leu	Ala	Glu	Leu	105	Pro	Val	Trp	Ser	110	Gln	Leu	Ile
			115					120					125			
Glu	Glu	His	Ser	Leu	Gln	Asp	Leu	Lys	Ala	Ser	Pro	Gln	Ala	Lys	Arg	
			130					135					140			
Leu	Asp	Ser	Val	Ser	Phe	Ala	His	Tyr	Cys	Glu	Lys	Glu	Leu	Asn	Leu	
			145			150					155				160	
Pro	Ala	Val	Leu	Gly	Val	Ala	Asn	Gln	Ile	Thr	Arg	Ala	Leu	Leu	Gly	
			165						170						175	
Val	Glu	Ala	His	Glu	Ile	Ser	Met	Leu	Phe	Leu	Thr	Asp	Tyr	Ile	Lys	
			180					185						190		
Ser	Ala	Thr	Gly	Leu	Ser	Asn	Ile	Phe	Ser	Asp	Lys	Lys	Asp	Gly	Gly	
			195				200					205				
Gln	Tyr	Val	Arg	Cys	Lys	Thr	Gly	Met	Gln	Ser	Ile	Cys	His	Ala	Met	
			210				215					220				
Ser	Lys	Glu	Leu	Val	Pro	Gly	Ser	Val	His	Leu	Asn	Thr	Pro	Val	Ala	
			225			230					235				240	
Glu	Ile	Glu	Gln	Ser	Ala	Ser	Gly	Cys	Thr	Val	Arg	Ser	Ala	Ser	Gly	
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Ala	Val	Phe	Arg	Ser	Lys	Lys	Val	Val	Val	Ser	Leu	Pro	Thr	Thr	Leu	
			260					265						270		
Tyr	Pro	Thr	Leu	Thr	Phe	Ser	Pro	Pro	Leu	Pro	Ala	Glu	Lys	Gln	Ala	
			275				280						285			
Leu	Ala	Glu	Asn	Ser	Ile	Leu	Gly	Tyr	Tyr	Ser	Lys	Ile	Val	Phe	Val	
			290			295					300					
Trp	Asp	Lys	Pro	Trp	Trp	Arg	Glu	Gln	Gly	Phe	Ser	Gly	Val	Leu	Gln	
			305			310				315					320	
Ser	Ser	Cys	Asp	Pro	Ile	Ser	Phe	Ala	Arg	Asp	Thr	Ser	Ile	Asp	Val	
			325					330						335		
Asp	Arg	Gln	Trp	Ser	Ile	Thr	Cys	Phe	Met	Val	Gly	Asp	Pro	Gly	Arg	
			340					345					350			
Lys	Trp	Ser	Gln	Gln	Ser	Lys	Gln	Val	Arg	Gln	Lys	Ser	Val	Trp	Asp	
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Gln	Leu	Arg	Ala	Ala	Tyr	Glu	Asn	Ala	Gly	Ala	Gln	Val	Pro	Glu	Pro	
			370			375					380					
Ala	Asn	Val	Leu	Glu	Ile	Glu	Trp	Ser	Lys	Gln	Gln	Tyr	Phe	Gln	Gly	
			385			390				395					400	
Ala	Pro	Ser	Ala	Val	Tyr	Gly	Leu	Asn	Asp	Leu	Ile	Thr	Leu	Gly	Ser	
			405					410						415		
Ala	Leu	Arg	Thr	Pro	Phe	Lys	Ser	Val	His	Phe	Val	Gly	Thr	Glu	Thr	
			420					425					430			
Ser	Leu	Val	Trp	Lys	Gly	Tyr	Met	Glu	Gly	Ala	Ile	Arg	Ser	Gly	Gln	
			435				440					445				
Arg	Gly	Ala	Ala	Glu	Val	Val	Ala	Ser	Leu	Val	Pro	Ala	Ala			
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<210> 9
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 <212> PRT
 <213> Exophiala spinifera

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 Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly Leu
 1 5 10 15
 Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu
 20 25 30
 Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly
 35 40 45
 Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp
 50 55 60
 Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu
 65 70 75 80

Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp
 85 90 95
 Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu
 100 105 110
 Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile
 115 120 125
 Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg
 130 135 140
 Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu
 145 150 155 160
 Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly
 165 170 175
 Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys
 180 185 190
 Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly
 195 200 205
 Gln Tyr Val Arg Cys Lys Thr Gly Ala Cys Gly Val Val Ser Gly Gly
 210 215 220
 Gly Leu Val Ser Gln Trp Ser Phe Gln Val Cys Ser Arg Phe Ala Met
 225 230 235 240
 Pro Cys Gln Arg Asn Leu Phe Gln Ala Gln Cys Thr Ser Thr Pro Pro
 245 250 255
 Ser Leu Lys Leu Ser Ser Arg His Pro Ala Val Gln Tyr Asp Arg Pro
 260 265 270
 Arg Ala Pro Cys Ser Glu Ala Lys Arg Trp Trp Phe Arg Tyr Arg Gln
 275 280 285
 Pro Cys Ile Pro Pro His Phe His His Leu Phe Pro Pro Arg Ser Lys
 290 295 300
 His Trp Arg Lys Ile Leu Ser Trp Ala Thr Ile Ala Arg Ser Ser Tyr
 305 310 315 320
 Gly Thr Ser Arg Gly Gly Ala Asn Lys Ala Ser Arg Ala Ser Ser Asn
 325 330 335
 Arg Ala Val Thr Pro Ser His Leu Pro Glu Ile Pro Ala Ser Thr Ser
 340 345 350
 Ile Asp Asn Gly Pro Leu Pro Val Ser Trp Ser Glu Thr Arg Asp Gly
 355 360 365
 Ser Gly Pro Asn Ser Pro Ser Arg Tyr Asp Lys Ser Leu Ser Gly Thr
 370 375 380
 Asn Ser Ala Gln Pro Thr Arg Thr Pro Gly Pro Lys Ser Gln Ser Arg
 385 390 395 400
 Pro Thr Cys Ser Lys Ser Ser Gly Arg Ser Ser Ser Ile Ser Lys Glu
 405 410 415
 Leu Arg Ala Pro Ser Met Gly Thr Ile Ser Ser His Trp Val Arg Arg
 420 425 430
 Ser Glu Arg Arg Ser Arg Val Phe Ile Ser Leu Glu Arg Arg Leu
 435 440 445
 Phe Gly Lys Gly Ile Trp Lys Gly Pro Tyr
 450 455

<210> 10
 <211> 1392
 <212> DNA
 <213> Exophiala spinifera

<220>
 <221> CDS
 <222> (1)...(1389)

<221> misc_feature
 <222> (1)...(3)
 <223> Extra lysine in K:trAPAO

<400> 10

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Lys Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly	
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ttg gag acg gca cgc aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt	96
Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val	
20 25 30	
ctt gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tgc	144
Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser	
35 40 45	
ggt ccc ggc agg acg act atc aac gac ctc ggc gct gcg tgg atc aat	192
Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn	
50 55 60	
gac agc aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg	240
Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu	
65 70 75 80	
gag ggc gag ctc cag agg acg act gga aat tca atc cat caa gca caa	288
Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln	
85 90 95	
gac ggt aca acc act aca gct cct tat ggt gac tcc ttg ctg agc gag	336
Asp Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu	
100 105 110	
gag gtt gca agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg	384
Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu	
115 120 125	
atc gaa gag cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag	432
Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys	
130 135 140	
cgg ctc gac agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac	480
Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn	
145 150 155 160	
ttg cct gct gtt ctc ggc gta gca aac cag atc aca cgc gct ctg ctc	528
Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu	
165 170 175	
ggt gtg gaa gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc	576
Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile	
180 185 190	
aag agt gcc acc ggt ctc agt aat att ttc tcg gac aag aaa gac ggc	624
Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly	
195 200 205	
ggg cag tat atg cga tgc aaa aca ggt atg cag tcg att tgc cat gcc	672
Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala	
210 215 220	
atg tca aag gaa ctt gtt cca ggc tca gtg cac ctc aac acc ccc gtc	720
Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val	
225 230 235 240	

gct gaa att gag cag tcg gca tcc ggc tgt aca gta cga tcg gcc tcg Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser 245 250 255	768
ggc gcc gtg ttc cga agc aaa aag gtg gtg gtt tcg tta ccg aca acc Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr 260 265 270	816
ttg tat ccc acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln 275 280 285	864
gca ttg gcg gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe 290 295 300	912
gta tgg gac aag ccg tgg tgg cgc gaa caa ggc ttc tcg gcc gtc ctc Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu 305 310 315 320	960
caa tcg agc tgt gac ccc atc tca ttt gcc aga gat acc agc atc gac Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp 325 330 335	1008
gtc gat cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly 340 345 350	1056
cgg aag tgg tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp 355 360 365	1104
gac caa ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu 370 375 380	1152
ccg gcc aac gtg ctc gaa atc gag tgg tcg aag cag cag tat ttc caa Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln 385 390 395 400	1200
gga gct ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly 405 410 415	1248
tcg gcg ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu 420 425 430	1296
acg tct tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tcg ggt Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly 435 440 445	1344
caa cga ggt gct gca gaa gtt gtg gct agc ctg gtg cca gca gca Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala 450 455 460	1389
tag	1392

<210> 11
 <211> 463
 <212> PRT
 <213> Exophiala spinifera

<400> 11

Lys	Asp	Asn	Val	Ala	Asp	Val	Val	Val	Val	Gly	Ala	Gly	Leu	Ser	Gly
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Leu	Glu	Thr	Ala	Arg	Lys	Val	Gln	Ala	Ala	Gly	Leu	Ser	Cys	Leu	Val
			20				25						30		
Leu	Glu	Ala	Met	Asp	Arg	Val	Gly	Gly	Lys	Thr	Leu	Ser	Val	Gln	Ser
		35					40					45			
Gly	Pro	Gly	Arg	Thr	Thr	Ile	Asn	Asp	Leu	Gly	Ala	Ala	Trp	Ile	Asn
	50					55					60				
Asp	Ser	Asn	Gln	Ser	Glu	Val	Ser	Arg	Leu	Phe	Glu	Arg	Phe	His	Leu
65					70					75					80
Glu	Gly	Glu	Leu	Gln	Arg	Thr	Thr	Gly	Asn	Ser	Ile	His	Gln	Ala	Gln
				85					90					95	
Asp	Gly	Thr	Thr	Thr	Thr	Ala	Pro	Tyr	Gly	Asp	Ser	Leu	Leu	Ser	Glu
			100					105					110		
Glu	Val	Ala	Ser	Ala	Leu	Ala	Glu	Leu	Leu	Pro	Val	Trp	Ser	Gln	Leu
		115					120					125			
Ile	Glu	Glu	His	Ser	Leu	Gln	Asp	Leu	Lys	Ala	Ser	Pro	Gln	Ala	Lys
	130					135					140				
Arg	Leu	Asp	Ser	Val	Ser	Phe	Ala	His	Tyr	Cys	Glu	Lys	Glu	Leu	Asn
145					150					155					160
Leu	Pro	Ala	Val	Leu	Gly	Val	Ala	Asn	Gln	Ile	Thr	Arg	Ala	Leu	Leu
			165					170						175	
Gly	Val	Glu	Ala	His	Glu	Ile	Ser	Met	Leu	Phe	Leu	Thr	Asp	Tyr	Ile
		180						185					190		
Lys	Ser	Ala	Thr	Gly	Leu	Ser	Asn	Ile	Phe	Ser	Asp	Lys	Lys	Asp	Gly
	195						200					205			
Gly	Gln	Tyr	Met	Arg	Cys	Lys	Thr	Gly	Met	Gln	Ser	Ile	Cys	His	Ala
	210					215					220				
Met	Ser	Lys	Glu	Leu	Val	Pro	Gly	Ser	Val	His	Leu	Asn	Thr	Pro	Val
225					230					235					240
Ala	Glu	Ile	Glu	Gln	Ser	Ala	Ser	Gly	Cys	Thr	Val	Arg	Ser	Ala	Ser
			245						250					255	
Gly	Ala	Val	Phe	Arg	Ser	Lys	Lys	Val	Val	Val	Ser	Leu	Pro	Thr	Thr
		260						265					270		
Leu	Tyr	Pro	Thr	Leu	Thr	Phe	Ser	Pro	Pro	Leu	Pro	Ala	Glu	Lys	Gln
	275						280					285			
Ala	Leu	Ala	Glu	Asn	Ser	Ile	Leu	Gly	Tyr	Tyr	Ser	Lys	Ile	Val	Phe
	290					295					300				
Val	Trp	Asp	Lys	Pro	Trp	Trp	Arg	Glu	Gln	Gly	Phe	Ser	Gly	Val	Leu
305					310					315					320
Gln	Ser	Ser	Cys	Asp	Pro	Ile	Ser	Phe	Ala	Arg	Asp	Thr	Ser	Ile	Asp
			325						330					335	
Val	Asp	Arg	Gln	Trp	Ser	Ile	Thr	Cys	Phe	Met	Val	Gly	Asp	Pro	Gly
			340					345					350		
Arg	Lys	Trp	Ser	Gln	Gln	Ser	Lys	Gln	Val	Arg	Gln	Lys	Ser	Val	Trp
	355						360					365			
Asp	Gln	Leu	Arg	Ala	Ala	Tyr	Glu	Asn	Ala	Gly	Ala	Gln	Val	Pro	Glu
	370					375					380				
Pro	Ala	Asn	Val	Leu	Glu	Ile	Glu	Trp	Ser	Lys	Gln	Gln	Tyr	Phe	Gln
385					390					395					400
Gly	Ala	Pro	Ser	Ala	Val	Tyr	Gly	Leu	Asn	Asp	Leu	Ile	Thr	Leu	Gly
			405						410					415	
Ser	Ala	Leu	Arg	Thr	Pro	Phe	Lys	Ser	Val	His	Phe	Val	Gly	Thr	Glu
		420					425						430		
Thr	Ser	Leu	Val	Trp	Lys	Gly	Tyr	Met	Glu	Gly	Ala	Ile	Arg	Ser	Gly
		435					440					445			
Gln	Arg	Gly	Ala	Ala	Glu	Val	Val	Ala	Ser	Leu	Val	Pro	Ala	Ala	
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<210> 12

<211> 34
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer sequence designed for cloning DNA into
 expression vectors, N23256

 <400> 12
 ggggaattca aagacaacgt tgcggacgtg gtag 34

 <210> 13
 <211> 34
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Primer sequence designed for cloning DNA into
 expression vectors, N23259

 <400> 13
 ggggcggccg cctatgctgc tggcaccagg ctag 34

 <210> 14
 <211> 29
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Designed oligonucleotide for 3' RACE, N21965

 <400> 14
 tggtttctgt accgacaacc ttgtatccc 29

 <210> 15
 <211> 28
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Designed oligonucleotide for 5' race, N21968

 <400> 15
 gagttggtcc cagacagact tttgtcgt 28

 <210> 16
 <211> 1673
 <212> DNA
 <213> Exophiala spinifera

 <220>
 <221> sig_peptide
 <222> (1)...(267)
 <223> yeast alpha mating factor secretion signal.

 <221> CDS
 <222> (1)...(1662)

 <400> 16
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				-85					-80					-75			
gca	tta	gct	gct	cca	gtc	aac	act	aca	aca	gaa	gat	gaa	acg	gca	caa		96
Ala	Leu	Ala	Ala	Pro	Val	Asn	Thr	Thr	Thr	Glu	Asp	Glu	Thr	Ala	Gln		
			-70					-65				-60					
att	ccg	gct	gaa	gct	gtc	atc	ggg	tac	tca	gat	tta	gaa	ggg	gat	ttc		144
Ile	Pro	Ala	Glu	Ala	Val	Ile	Gly	Tyr	Ser	Asp	Leu	Glu	Gly	Asp	Phe		
	-55						-50				-45						
gat	gtt	gct	gtt	ttg	cca	ttt	tcc	aac	agc	aca	aat	aac	ggg	tta	ttg		192
Asp	Val	Ala	Val	Leu	Pro	Phe	Ser	Asn	Ser	Thr	Asn	Asn	Gly	Leu	Leu		
	-40					-35				-30							
ttt	ata	aat	act	act	att	gcc	agc	att	gct	gct	aaa	gaa	gaa	ggg	gta		240
Phe	Ile	Asn	Thr	Thr	Ile	Ala	Ser	Ile	Ala	Ala	Lys	Glu	Glu	Gly	Val		
	-25				-20				-15					-10			
tct	ctc	gag	aaa	aga	gag	gct	gaa	gct	gaa	ttc	aaa	gac	aac	gtt	gcg		288
Ser	Leu	Glu	Lys	Arg	Glu	Ala	Glu	Ala	Glu	Phe	Lys	Asp	Asn	Val	Ala		
			-5					1				5					
gac	gtg	gta	gtg	gtg	ggc	gct	ggc	ttg	agc	ggg	ttg	gag	acg	gca	cg		336
Asp	Val	Val	Val	Val	Gly	Ala	Gly	Leu	Ser	Gly	Leu	Glu	Thr	Ala	Arg		
		10				15					20						
aaa	gtc	cag	gcc	gcc	ggg	ctg	tcc	tgc	ctc	gtt	ctt	gag	gcg	atg	gat		384
Lys	Val	Gln	Ala	Ala	Gly	Leu	Ser	Cys	Leu	Val	Leu	Glu	Ala	Met	Asp		
	25				30					35							
cgt	gta	ggg	gga	aag	act	ctg	agc	gta	caa	tcg	ggg	ccc	ggc	agg	acg		432
Arg	Val	Gly	Gly	Lys	Thr	Leu	Ser	Val	Gln	Ser	Gly	Pro	Gly	Arg	Thr		
	40				45				50					55			
act	atc	aac	gac	ctc	ggc	gct	gcg	tgg	atc	aat	gac	agc	aac	caa	agc		480
Thr	Ile	Asn	Asp	Leu	Gly	Ala	Ala	Trp	Ile	Asn	Asp	Ser	Asn	Gln	Ser		
				60					65					70			
gaa	gta	tcc	aga	ttg	ttt	gaa	aga	ttt	cat	ttg	gag	ggc	gag	ctc	cag		528
Glu	Val	Ser	Arg	Leu	Phe	Glu	Arg	Phe	His	Leu	Glu	Gly	Glu	Leu	Gln		
			75					80					85				
agg	acg	act	gga	aat	tca	atc	cat	caa	gca	caa	gac	ggg	aca	acc	act		576
Arg	Thr	Thr	Gly	Asn	Ser	Ile	His	Gln	Ala	Gln	Asp	Gly	Thr	Thr	Thr		
		90					95					100					
aca	gct	cct	tat	ggg	gac	tcc	ttg	ctg	agc	gag	gag	gtt	gca	agt	gca		624
Thr	Ala	Pro	Tyr	Gly	Asp	Ser	Leu	Leu	Ser	Glu	Glu	Val	Ala	Ser	Ala		
	105					110					115						
ctt	gcg	gaa	ctc	ctc	ccc	gta	tgg	tct	cag	ctg	atc	gaa	gag	cat	agc		672
Leu	Ala	Glu	Leu	Leu	Pro	Val	Trp	Ser	Gln	Leu	Ile	Glu	Glu	His	Ser		
	120					125				130				135			
ctt	caa	gac	ctc	aag	gcg	agc	cct	cag	gcg	aag	cgg	ctc	gac	agt	gtg		720
Leu	Gln	Asp	Leu	Lys	Ala	Ser	Pro	Gln	Ala	Lys	Arg	Leu	Asp	Ser	Val		
				140					145					150			
agc	ttc	gcg	cac	tac	tgt	gag	aag	gaa	cta	aac	ttg	cct	gct	gtt	ctc		768
Ser	Phe	Ala	His	Tyr	Cys	Glu	Lys	Glu	Leu	Asn	Leu	Pro	Ala	Val	Leu		
			155					160						165			

ggc gta gca aac cag atc aca cgc gct ctg ctc ggt gtg gaa gcc cac Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His 170 175 180	816
gag atc agc atg ctt ttt ctc acc gac tac atc aag agt gcc acc ggt Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly 185 190 195	864
ctc agt aat att ttc tcg gac aag aaa gac ggc ggg cag tat atg cga Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg 200 205 210 215	912
tgc aaa aca ggt atg cag tcg att tgc cat gcc atg tca aag gaa ctt Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu 220 225 230	960
gtt cca ggc tca gtg cac ctc aac acc ccc gtc gct gaa att gag cag Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln 235 240 245	1008
tcg gca tcc ggc tgt aca gta cga tcg gcc tcg ggc gcc gtg ttc cga Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg 250 255 260	1056
agc aaa aag gtg gtg gtt tcg tta ccg aca acc ttg tat ccc acc ttg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu 265 270 275	1104
aca ttt tca cca cct ctt ccc gcc gag aag caa gca ttg gcg gaa aat Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn 280 285 290 295	1152
tct atc ctg ggc tac tat agc aag ata gtc ttc gta tgg gac aag ccg Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro 300 305 310	1200
tgg tgg cgc gaa caa ggc ttc tcg ggc gtc ctc caa tcg agc tgt gac Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp 315 320 325	1248
ccc atc tca ttt gcc aga gat acc agc atc gac gtc gat cga caa tgg Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp 330 335 340	1296
tcc att acc tgt ttc atg gtc gga gac ccg gga cgg aag tgg tcc caa Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln 345 350 355	1344
cag tcc aag cag gta cga caa aag tct gtc tgg gac caa ctc cgc gca Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala 360 365 370 375	1392
gcc tac gag aac gcc ggg gcc caa gtc cca gag ccg gcc aac gtg ctc Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu 380 385 390	1440
gaa atc gag tgg tcg aag cag cag tat ttc caa gga gct ccg agc gcc Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala 395 400 405	1488
gtc tat ggg ctg aac gat ctc atc aca ctg ggt tcg gcg ctc aga acg	1536

Val	Tyr	Gly	Leu	Asn	Asp	Leu	Ile	Thr	Leu	Gly	Ser	Ala	Leu	Arg	Thr	
		410					415					420				
ccg	ttc	aag	agt	gtt	cat	ttc	gtt	gga	acg	gag	acg	tct	tta	gtt	tgg	1584
Pro	Phe	Lys	Ser	Val	His	Phe	Val	Gly	Thr	Glu	Thr	Ser	Leu	Val	Trp	
		425					430					435				
aaa	ggg	tat	atg	gaa	ggg	gcc	ata	cga	tcg	ggt	caa	cga	ggt	gct	gca	1632
Lys	Gly	Tyr	Met	Glu	Gly	Ala	Ile	Arg	Ser	Gly	Gln	Arg	Gly	Ala	Ala	
		440				445					450				455	
gaa	gtt	gtg	gct	agc	ctg	gtg	cca	gca	gca	taggcggccg	c					1673
Glu	Val	Val	Ala	Ser	Leu	Val	Pro	Ala	Ala							
					460				465							

<210> 17
 <211> 554
 <212> PRT
 <213> Exophiala spinifera

<220>
 <221> SIGNAL
 <222> (1)...(89)

<400> 17															
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			-70					-65					-60		
Ile	Pro	Ala	Glu	Ala	Val	Ile	Gly	Tyr	Ser	Asp	Leu	Glu	Gly	Asp	Phe
		-55					-50					-45			
Asp	Val	Ala	Val	Leu	Pro	Phe	Ser	Asn	Ser	Thr	Asn	Asn	Gly	Leu	Leu
	-40					-35				-30					
Phe	Ile	Asn	Thr	Thr	Ile	Ala	Ser	Ile	Ala	Ala	Lys	Glu	Glu	Gly	Val
	-25				-20				-15						-10
Ser	Leu	Glu	Lys	Arg	Glu	Ala	Glu	Ala	Glu	Phe	Lys	Asp	Asn	Val	Ala
			-5					1					5		
Asp	Val	Val	Val	Val	Gly	Ala	Gly	Leu	Ser	Gly	Leu	Glu	Thr	Ala	Arg
	10					15						20			
Lys	Val	Gln	Ala	Ala	Gly	Leu	Ser	Cys	Leu	Val	Leu	Glu	Ala	Met	Asp
	25					30					35				
Arg	Val	Gly	Gly	Lys	Thr	Leu	Ser	Val	Gln	Ser	Gly	Pro	Gly	Arg	Thr
	40				45				50					55	
Thr	Ile	Asn	Asp	Leu	Gly	Ala	Ala	Trp	Ile	Asn	Asp	Ser	Asn	Gln	Ser
		60						65						70	
Glu	Val	Ser	Arg	Leu	Phe	Glu	Arg	Phe	His	Leu	Glu	Gly	Glu	Leu	Gln
		75						80					85		
Arg	Thr	Thr	Gly	Asn	Ser	Ile	His	Gln	Ala	Gln	Asp	Gly	Thr	Thr	Thr
	90					95						100			
Thr	Ala	Pro	Tyr	Gly	Asp	Ser	Leu	Leu	Ser	Glu	Glu	Val	Ala	Ser	Ala
	105					110						115			
Leu	Ala	Glu	Leu	Leu	Pro	Val	Trp	Ser	Gln	Leu	Ile	Glu	Glu	His	Ser
	120				125					130				135	
Leu	Gln	Asp	Leu	Lys	Ala	Ser	Pro	Gln	Ala	Lys	Arg	Leu	Asp	Ser	Val
			140						145					150	
Ser	Phe	Ala	His	Tyr	Cys	Glu	Lys	Glu	Leu	Asn	Leu	Pro	Ala	Val	Leu
			155					160					165		
Gly	Val	Ala	Asn	Gln	Ile	Thr	Arg	Ala	Leu	Leu	Gly	Val	Glu	Ala	His
	170					175						180			
Glu	Ile	Ser	Met	Leu	Phe	Leu	Thr	Asp	Tyr	Ile	Lys	Ser	Ala	Thr	Gly
	185					190					195				

Leu	Ser	Asn	Ile	Phe	Ser	Asp	Lys	Lys	Asp	Gly	Gly	Gln	Tyr	Met	Arg
200					205					210					215
Cys	Lys	Thr	Gly	Met	Gln	Ser	Ile	Cys	His	Ala	Met	Ser	Lys	Glu	Leu
				220					225					230	
Val	Pro	Gly	Ser	Val	His	Leu	Asn	Thr	Pro	Val	Ala	Glu	Ile	Glu	Gln
			235					240					245		
Ser	Ala	Ser	Gly	Cys	Thr	Val	Arg	Ser	Ala	Ser	Gly	Ala	Val	Phe	Arg
	250						255					260			
Ser	Lys	Lys	Val	Val	Val	Ser	Leu	Pro	Thr	Thr	Leu	Tyr	Pro	Thr	Leu
	265					270					275				
Thr	Phe	Ser	Pro	Pro	Leu	Pro	Ala	Glu	Lys	Gln	Ala	Leu	Ala	Glu	Asn
280					285					290					295
Ser	Ile	Leu	Gly	Tyr	Tyr	Ser	Lys	Ile	Val	Phe	Val	Trp	Asp	Lys	Pro
			300						305					310	
Trp	Trp	Arg	Glu	Gln	Gly	Phe	Ser	Gly	Val	Leu	Gln	Ser	Ser	Cys	Asp
			315					320					325		
Pro	Ile	Ser	Phe	Ala	Arg	Asp	Thr	Ser	Ile	Asp	Val	Asp	Arg	Gln	Trp
	330					335						340			
Ser	Ile	Thr	Cys	Phe	Met	Val	Gly	Asp	Pro	Gly	Arg	Lys	Trp	Ser	Gln
	345					350					355				
Gln	Ser	Lys	Gln	Val	Arg	Gln	Lys	Ser	Val	Trp	Asp	Gln	Leu	Arg	Ala
360					365					370					375
Ala	Tyr	Glu	Asn	Ala	Gly	Ala	Gln	Val	Pro	Glu	Pro	Ala	Asn	Val	Leu
				380					385					390	
Glu	Ile	Glu	Trp	Ser	Lys	Gln	Gln	Tyr	Phe	Gln	Gly	Ala	Pro	Ser	Ala
			395					400					405		
Val	Tyr	Gly	Leu	Asn	Asp	Leu	Ile	Thr	Leu	Gly	Ser	Ala	Leu	Arg	Thr
	410					415						420			
Pro	Phe	Lys	Ser	Val	His	Phe	Val	Gly	Thr	Glu	Thr	Ser	Leu	Val	Trp
	425					430					435				
Lys	Gly	Tyr	Met	Glu	Gly	Ala	Ile	Arg	Ser	Gly	Gln	Arg	Gly	Ala	Ala
440					445					450					455
Glu	Val	Val	Ala	Ser	Leu	Val	Pro	Ala	Ala						
				460				465							

<210> 18
 <211> 2079
 <212> DNA
 <213> Unknown

<220>
 <223> GST:K:trAPAO 2079 nt. Translation starting at nt 1
 - 687, gst fusion + polylinker, 688-2076,
 K:trAPAO, extra lysine underlined; 2077-2079, stop
 codon. For bacterial expression.

<221> CDS
 <222> (1)...(2076)

<221> misc_feature
 <222> (1)...(687)
 <223> gst fusion + polylinker

<221> misc_feature
 <222> (688)...(2076)
 <223> K:trAPAO

<221> misc_feature
 <222> (688)...(690)
 <223> Extra lysine

<400> 18

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Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro	
1 5 10 15	
act cga ctt ctt ttg gaa tat ctt gaa gaa aaa tat gaa gag cat ttg	96
Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu	
20 25 30	
tat gag cgc gat gaa ggt gat aaa tgg cga aac aaa aag ttt gaa ttg	144
Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu	
35 40 45	
ggg ttg gag ttt ccc aat ctt cct tat tat att gat ggt gat gtt aaa	192
Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys	
50 55 60	
tta aca cag tct atg gcc atc ata cgt tat ata gct gac aag cac aac	240
Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn	
65 70 75 80	
atg ttg ggt ggt tgt cca aaa gag cgt gca gag att tca atg ctt gaa	288
Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu	
85 90 95	
gga gcg gtt ttg gat att aga tac ggt gtt tcg aga att gca tat agt	336
Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser	
100 105 110	
aaa gac ttt gaa act ctc aaa gtt gat ttt ctt agc aag cta cct gaa	384
Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu	
115 120 125	
atg ctg aaa atg ttc gaa gat cgt tta tgt cat aaa aca tat tta aat	432
Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn	
130 135 140	
ggg gat cat gta acc cat cct gac ttc atg ttg tat gac gct ctt gat	480
Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp	
145 150 155 160	
gtt gtt tta tac atg gac cca atg tgc ctg gat gcg ttc cca aaa tta	528
Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu	
165 170 175	
gtt tgt ttt aaa aaa cgt att gaa gct atc cca caa att gat aag tac	576
Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr	
180 185 190	
ttg aaa tcc agc aag tat ata gca tgg cct ttg cag ggc tgg caa gcc	624
Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala	
195 200 205	
acg ttt ggt ggt ggc gac cat cct cca aaa tcg gat ctg gtt ccg cgt	672
Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg	
210 215 220	
gga tcc ccg gaa ttc aaa gac aac gtt gcg gac gtg gta gtg gtg ggc	720
Gly Ser Pro Glu Phe Lys Asp Asn Val Ala Asp Val Val Val Val Gly	
225 230 235 240	
gct ggc ttg agc ggt ttg gag acg gca cgc aaa gtc cag gcc gcc ggt	768

Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly	
245 250 255	
ctg tcc tgc ctc gtt ctt gag gcg atg gat cgt gta ggg gga aag act	816
Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr	
260 265 270	
ctg agc gta caa tcg ggt ccc ggc agg acg act atc aac gac ctc ggc	864
Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly	
275 280 285	
gct gcg tgg atc aat gac agc aac caa agc gaa gta tcc aga ttg ttt	912
Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe	
290 295 300	
gaa aga ttt cat ttg gag ggc gag ctc cag agg acg act gga aat tca	960
Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser	
305 310 315 320	
atc cat caa gca caa gac ggt aca acc act aca gct cct tat ggt gac	1008
Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp	
325 330 335	
tcc ttg ctg agc gag gag gtt gca agt gca ctt gcg gaa ctc ctc ccc	1056
Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro	
340 345 350	
gta tgg tct cag ctg atc gaa gag cat agc ctt caa gac ctc aag gcg	1104
Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala	
355 360 365	
agc cct cag gcg aag cgg ctc gac agt gtg agc ttc gcg cac tac tgt	1152
Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys	
370 375 380	
gag aag gaa cta aac ttg cct gct gtt ctc ggc gta gca aac cag atc	1200
Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile	
385 390 395 400	
aca cgc gct ctg ctc ggt gtg gaa gcc cac gag atc agc atg ctt ttt	1248
Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser Met Leu Phe	
405 410 415	
ctc acc gac tac atc aag agt gcc acc ggt ctc agt aat att ttc tcg	1296
Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser	
420 425 430	
gac aag aaa gac ggc ggg cag tat atg cga tgc aaa aca ggt atg cag	1344
Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln	
435 440 445	
tcg att tgc cat gcc atg tca aag gaa ctt gtt cca ggc tca gtg cac	1392
Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro Gly Ser Val His	
450 455 460	
ctc aac acc ccc gtc gct gaa att gag cag tcg gca tcc ggc tgt aca	1440
Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr	
465 470 475 480	
gta cga tcg gcc tcg ggc gcc gtg ttc cga agc aaa aag gtg gtg gtt	1488
Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys Lys Val Val Val	
485 490 495	

tcg tta ccg aca acc ttg tat ccc acc ttg aca ttt tca cca cct ctt	1536
Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu	
500 505 510	

ccc gcc gag aag caa gca ttg gcg gaa aat tct atc ctg ggc tac tat	1584
Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr	
515 520 525	

agc aag ata gtc ttc gta tgg gac aag ccg tgg tgg cgc gaa caa ggc	1632
Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly	
530 535 540	

ttc tcg ggc gtc ctc caa tcg agc tgt gac ccc atc tca ttt gcc aga	1680
Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg	
545 550 555 560	

gat acc agc atc gac gtc gat cga caa tgg tcc att acc tgt ttc atg	1728
Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met	
565 570 575	

gtc gga gac ccg gga cgg aag tgg tcc caa cag tcc aag cag gta cga	1776
Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg	
580 585 590	

caa aag tct gtc tgg gac caa ctc cgc gca gcc tac gag aac gcc ggg	1824
Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly	
595 600 605	

gcc caa gtc cca gag ccg gcc aac gtg ctc gaa atc gag tgg tcg aag	1872
Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys	
610 615 620	

cag cag tat ttc caa gga gct ccg agc gcc gtc tat ggg ctg aac gat	1920
Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp	
625 630 635 640	

ctc atc aca ctg ggt tcg gcg ctc aga acg ccg ttc aag agt gtt cat	1968
Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His	
645 650 655	

ttc gtt gga acg gag acg tct tta gtt tgg aaa ggg tat atg gaa ggg	2016
Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly	
660 665 670	

gcc ata cga tcg ggt caa cga ggt gct gca gaa gtt gtg gct agc ctg	2064
Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu	
675 680 685	

gtg cca gca gca tag	2079
Val Pro Ala Ala	
690	

<210> 19
 <211> 692
 <212> PRT
 <213> Unknown

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Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu
 20 25 30
 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
 35 40 45
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
 50 55 60
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
 65 70 75 80
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
 85 90 95
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser
 100 105 110
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu
 115 120 125
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn
 130 135 140
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp
 145 150 155 160
 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
 165 170 175
 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
 180 185 190
 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
 195 200 205
 Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
 210 215 220
 Gly Ser Pro Glu Phe Lys Asp Asn Val Ala Asp Val Val Val Val Gly
 225 230 235 240
 Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly
 245 250 255
 Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr
 260 265 270
 Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly
 275 280 285
 Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe
 290 295 300
 Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser
 305 310 315 320
 Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp
 325 330 335
 Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro
 340 345 350
 Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala
 355 360 365
 Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys
 370 375 380
 Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile
 385 390 395 400
 Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser Met Leu Phe
 405 410 415
 Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser
 420 425 430
 Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln
 435 440 445
 Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro Gly Ser Val His
 450 455 460
 Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr
 465 470 475 480
 Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys Lys Val Val Val
 485 490 495
 Ser Leu Pro Thr Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu
 500 505 510

Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr
 515 520 525
 Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly
 530 535 540
 Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg
 545 550 555 560
 Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met
 565 570 575
 Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg
 580 585 590
 Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly
 595 600 605
 Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys
 610 615 620
 Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp
 625 630 635 640
 Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His
 645 650 655
 Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly
 660 665 670
 Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu
 675 680 685
 Val Pro Ala Ala
 690

<210> 20
 <211> 1464
 <212> DNA
 <213> Unknown

<220>
 <223> Nucleotide sequence of K:trAPAO translational
 fusion with barley alpha amylase signal sequence,
 for expression and secretion of the mature trAPAO
 in maize. Nucleotides 1-72, barley alpha amylase
 signal sequence, nucleotides 73-75, added lysine
 residue; nucleotides 76 -1464 , trAPAO cDNA.

<221> sig_peptide
 <222> (1)...(72)
 <223> Barley alpha amylase signal sequence

<221> misc_feature
 <222> (73)...(1464)
 <223> K:trAPAOcDNA

<221> CDS
 <222> (1)...(1461)

<221> misc_feature
 <222> (73)...(75)
 <223> Added lysine residue

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 Met Ala Asn Lys His Leu Ser Leu Ser Leu Phe Leu Val Leu Leu Gly
 -20 -15 -10
 ctc tcc gcc tcc ctc gcc agc ggc aaa gac aac gtt gcg gac gtg gta 96
 Leu Ser Ala Ser Leu Ala Ser Gly Lys Asp Asn Val Ala Asp Val Val
 -5 1 5

gtg gtg ggc gct ggc ttg agc ggt ttg gag acg gca cgc aaa gtc cag	144
Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln	
10 15 20	
gcc gcc ggt ctg tcc tgc ctc gtt ctt gag gcg atg gat cgt gta ggg	192
Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly	
25 30 35 40	
gga aag act ctg agc gta caa tgc ggt ccc ggc agg acg act atc aac	240
Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile Asn	
45 50 55	
gac ctc ggc gct gcg tgg atc aat gac agc aac caa agc gaa gta tcc	288
Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Ser	
60 65 70	
aga ttg ttt gaa aga ttt cat ttg gag ggc gag ctc cag agg acg act	336
Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr Thr	
75 80 85	
gga aat tca atc cat caa gca caa gac ggt aca acc act aca gct cct	384
Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala Pro	
90 95 100	
tat ggt gac tcc ttg ctg agc gag gag gtt gca agt gca ctt gcg gaa	432
Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu	
105 110 115 120	
ctc ctc ccc gta tgg tct cag ctg atc gaa gag cat agc ctt caa gac	480
Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln Asp	
125 130 135	
ctc aag gcg agc cct cag gcg aag cgg ctc gac agt gtg agc ttc gcg	528
Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe Ala	
140 145 150	
cac tac tgt gag aag gaa cta aac ttg cct gct gtt ctc ggc gta gca	576
His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val Ala	
155 160 165	
aac cag atc aca cgc gct ctg ctc ggt gtg gaa gcc cac gag atc agc	624
Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser	
170 175 180	
atg ctt ttt ctc acc gac tac atc aag agt gcc acc ggt ctc agt aat	672
Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn	
185 190 195 200	
att ttc tgc gac aag aaa gac ggc ggg cag tat atg cga tgc aaa aca	720
Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr	
205 210 215	
ggt atg cag tgc att tgc cat gcc atg tca aag gaa ctt gtt cca ggc	768
Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro Gly	
220 225 230	
tca gtg cac ctc aac acc ccc gtc gct gaa att gag cag tgc gca tcc	816
Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser	
235 240 245	
ggc tgt aca gta cga tgc gcc tgc ggc gcc gtg ttc cga agc aaa aag	864

Gly	Cys	Thr	Val	Arg	Ser	Ala	Ser	Gly	Ala	Val	Phe	Arg	Ser	Lys	Lys	
250						255					260					
gtg	gtg	gtt	tcg	tta	ccg	aca	acc	ttg	tat	ccc	acc	ttg	aca	ttt	tca	912
Val	Val	Val	Ser	Leu	Pro	Thr	Thr	Leu	Tyr	Pro	Thr	Leu	Thr	Phe	Ser	
265					270					275					280	
cca	cct	ctt	ccc	gcc	gag	aag	caa	gca	ttg	gcg	gaa	aat	tct	atc	ctg	960
Pro	Pro	Leu	Pro	Ala	Glu	Lys	Gln	Ala	Leu	Ala	Glu	Asn	Ser	Ile	Leu	
				285					290					295		
ggc	tac	tat	agc	aag	ata	gtc	ttc	gta	tgg	gac	aag	ccg	tgg	tgg	cgc	1008
Gly	Tyr	Tyr	Ser	Lys	Ile	Val	Phe	Val	Trp	Asp	Lys	Pro	Trp	Trp	Arg	
			300					305					310			
gaa	caa	ggc	ttc	tcg	ggc	gtc	ctc	caa	tcg	agc	tgt	gac	ccc	atc	tca	1056
Glu	Gln	Gly	Phe	Ser	Gly	Val	Leu	Gln	Ser	Ser	Cys	Asp	Pro	Ile	Ser	
		315					320					325				
ttt	gcc	aga	gat	acc	agc	atc	gac	gtc	gat	cga	caa	tgg	tcc	att	acc	1104
Phe	Ala	Arg	Asp	Thr	Ser	Ile	Asp	Val	Asp	Arg	Gln	Trp	Ser	Ile	Thr	
	330					335					340					
tgt	ttc	atg	gtc	gga	gac	ccg	gga	cgg	aag	tgg	tcc	caa	cag	tcc	aag	1152
Cys	Phe	Met	Val	Gly	Asp	Pro	Gly	Arg	Lys	Trp	Ser	Gln	Gln	Ser	Lys	
345					350					355					360	
cag	gta	cga	caa	aag	tct	gtc	tgg	gac	caa	ctc	cgc	gca	gcc	tac	gag	1200
Gln	Val	Arg	Gln	Lys	Ser	Val	Trp	Asp	Gln	Leu	Arg	Ala	Ala	Tyr	Glu	
				365					370					375		
aac	gcc	ggg	gcc	caa	gtc	cca	gag	ccg	gcc	aac	gtg	ctc	gaa	atc	gag	1248
Asn	Ala	Gly	Ala	Gln	Val	Pro	Glu	Pro	Ala	Asn	Val	Leu	Glu	Ile	Glu	
			380					385					390			
tgg	tcg	aag	cag	cag	tat	ttc	caa	gga	gct	ccg	agc	gcc	gtc	tat	ggg	1296
Trp	Ser	Lys	Gln	Gln	Tyr	Phe	Gln	Gly	Ala	Pro	Ser	Ala	Val	Tyr	Gly	
		395					400					405				
ctg	aac	gat	ctc	atc	aca	ctg	ggt	tcg	gcg	ctc	aga	acg	ccg	ttc	aag	1344
Leu	Asn	Asp	Leu	Ile	Thr	Leu	Gly	Ser	Ala	Leu	Arg	Thr	Pro	Phe	Lys	
	410					415					420					
agt	gtt	cat	ttc	gtt	gga	acg	gag	acg	tct	tta	gtt	tgg	aaa	ggg	tat	1392
Ser	Val	His	Phe	Val	Gly	Thr	Glu	Thr	Ser	Leu	Val	Trp	Lys	Gly	Tyr	
425					430					435					440	
atg	gaa	ggg	gcc	ata	cga	tcg	ggt	caa	cga	ggt	gct	gca	gaa	gtt	gtg	1440
Met	Glu	Gly	Ala	Ile	Arg	Ser	Gly	Gln	Arg	Gly	Ala	Ala	Glu	Val	Val	
				445					450					455		
gct	agc	ctg	gtg	cca	gca	gca	tag									1464
Ala	Ser	Leu	Val	Pro	Ala	Ala										
				460												

<210> 21
 <211> 487
 <212> PRT
 <213> Unknown

25

425		430		435		440									
Met	Glu	Gly	Ala	Ile	Arg	Ser	Gly	Gln	Arg	Gly	Ala	Ala	Glu	Val	Val
			445					450						455	
Ala	Ser	Leu	Val	Pro	Ala	Ala									
			460												

<210> 22
 <211> 1803
 <212> DNA
 <213> *Exophiala spinifera*

<220>
 <221> CDS
 <222> (1)...(1800)

<400> 22	
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Met Ala Leu Ala Pro Ser Tyr Ile Asn Pro Pro Asn Val Ala Ser Pro	
1 5 10 15	
gca ggg tat tct cac gtc ggc gta ggc cca gac gga ggg agg tat gtg	96
Ala Gly Tyr Ser His Val Gly Val Gly Pro Asp Gly Gly Arg Tyr Val	
20 25 30	
aca ata gct gga cag att gga caa gac gct tcg ggc gtg aca gac cct	144
Thr Ile Ala Gly Gln Ile Gly Gln Asp Ala Ser Gly Val Thr Asp Pro	
35 40 45	
gcc tac gag aaa cag gtt gcc caa gca ttc gcc aat ctg cga gct tgc	192
Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys	
50 55 60	
ctt gct gca gtt gga gcc act tca aac gac gtc acc aag ctc aat tac	240
Leu Ala Ala Val Gly Ala Thr Ser Asn Asp Val Thr Lys Leu Asn Tyr	
65 70 75 80	
tac atc gtc gac tac gcc ccg agc aaa ctc acc gca att gga gat ggg	288
Tyr Ile Val Asp Tyr Ala Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly	
85 90 95	
ctg aag gct acc ttt gcc ctt gac agg ctc cct cct tgc acg ctg gtg	336
Leu Lys Ala Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val	
100 105 110	
cca gtg tcg gcc ttg tct tca cct gaa tac ctc ttt gag gtt gat gcc	384
Pro Val Ser Ala Leu Ser Ser Pro Glu Tyr Leu Phe Glu Val Asp Ala	
115 120 125	
acg gcg ctg gtg ccg gga cac acg acc cca gac aac gtt gcg gac gtg	432
Thr Ala Leu Val Pro Gly His Thr Thr Pro Asp Asn Val Ala Asp Val	
130 135 140	
gta gtg gtg ggc gct ggc ttg agc ggt ttg gag acg gca cgc aaa gtc	480
Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val	
145 150 155 160	
cag gcc gcc ggt ctg tcc tgc ctc gtt ctt gag gcg atg gat cgt gta	528
Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val	
165 170 175	
ggg gga aag act ctg agc gta caa tcg ggt ccc ggc agg acg act atc	576
Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile	

ctg ggc tac tat agc aag ata gtc ttc gta tgg gac aag ccg tgg tgg	1344
Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp	
435 440 445	
cgc gaa caa ggc ttc tcg ggc gtc ctc caa tcg agc tgt gac ccc atc	1392
Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile	
450 455 460	
tca ttt gcc aga gat acc agc atc gac gtc gat cga caa tgg tcc att	1440
Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Arg Gln Trp Ser Ile	
465 470 475 480	
acc tgt ttc atg gtc gga gac ccg gga cgg aag tgg tcc caa cag tcc	1488
Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser	
485 490 495	
aag cag gta cga caa aag tct gtc tgg gac caa ctc cgc gca gcc tac	1536
Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr	
500 505 510	
gag aac gcc ggg gcc caa gtc cca gag ccg gcc aac gtg ctc gaa atc	1584
Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile	
515 520 525	
gag tgg tcg aag cag cag tat ttc caa gga gct ccg agc gcc gtc tat	1632
Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr	
530 535 540	
ggg ctg aac gat ctc atc aca ctg ggt tcg gcg ctc aga acg ccg ttc	1680
Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe	
545 550 555 560	
aag agt gtt cat ttc gtt gga acg gag acg tct tta gtt tgg aaa ggg	1728
Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly	
565 570 575	
tat atg gaa ggg gcc ata cga tcg ggt caa cga ggt gct gca gaa gtt	1776
Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val	
580 585 590	
gtg gct agc ctg gtg cca gca gca tag	1803
Val Ala Ser Leu Val Pro Ala Ala	
595 600	

<210> 23

<211> 600

<212> PRT

<213> *Exophiala spinifera*

<400> 23

Met Ala Leu Ala Pro Ser Tyr Ile Asn Pro Pro Asn Val Ala Ser Pro	
1 5 10 15	
Ala Gly Tyr Ser His Val Gly Val Gly Pro Asp Gly Gly Arg Tyr Val	
20 25 30	
Thr Ile Ala Gly Gln Ile Gly Gln Asp Ala Ser Gly Val Thr Asp Pro	
35 40 45	
Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys	
50 55 60	
Leu Ala Ala Val Gly Ala Thr Ser Asn Asp Val Thr Lys Leu Asn Tyr	
65 70 75 80	
Tyr Ile Val Asp Tyr Ala Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly	

				85					90				95				
Leu	Lys	Ala	Thr	Phe	Ala	Leu	Asp	Arg	Leu	Pro	Pro	Cys	Thr	Leu	Val		
			100					105					110				
Pro	Val	Ser	Ala	Leu	Ser	Ser	Pro	Glu	Tyr	Leu	Phe	Glu	Val	Asp	Ala		
		115					120					125					
Thr	Ala	Leu	Val	Pro	Gly	His	Thr	Thr	Pro	Asp	Asn	Val	Ala	Asp	Val		
	130					135					140						
Val	Val	Val	Gly	Ala	Gly	Leu	Ser	Gly	Leu	Glu	Thr	Ala	Arg	Lys	Val		
145					150					155					160		
Gln	Ala	Ala	Gly	Leu	Ser	Cys	Leu	Val	Leu	Glu	Ala	Met	Asp	Arg	Val		
			165						170				175				
Gly	Gly	Lys	Thr	Leu	Ser	Val	Gln	Ser	Gly	Pro	Gly	Arg	Thr	Thr	Ile		
			180					185					190				
Asn	Asp	Leu	Gly	Ala	Ala	Trp	Ile	Asn	Asp	Ser	Asn	Gln	Ser	Glu	Val		
	195						200					205					
Ser	Arg	Leu	Phe	Glu	Arg	Phe	His	Leu	Glu	Gly	Glu	Leu	Gln	Arg	Thr		
	210					215					220						
Thr	Gly	Asn	Ser	Ile	His	Gln	Ala	Gln	Asp	Gly	Thr	Thr	Thr	Thr	Ala		
225				230					235						240		
Pro	Tyr	Gly	Asp	Ser	Leu	Leu	Ser	Glu	Glu	Val	Ala	Ser	Ala	Leu	Ala		
			245						250					255			
Glu	Leu	Leu	Pro	Val	Trp	Ser	Gln	Leu	Ile	Glu	Glu	His	Ser	Leu	Gln		
			260				265						270				
Asp	Leu	Lys	Ala	Ser	Pro	Gln	Ala	Lys	Arg	Leu	Asp	Ser	Val	Ser	Phe		
	275						280					285					
Ala	His	Tyr	Cys	Glu	Lys	Glu	Leu	Asn	Leu	Pro	Ala	Val	Leu	Gly	Val		
	290					295					300						
Ala	Asn	Gln	Ile	Thr	Arg	Ala	Leu	Leu	Gly	Val	Glu	Ala	His	Glu	Ile		
305					310					315					320		
Ser	Met	Leu	Phe	Leu	Thr	Asp	Tyr	Ile	Lys	Ser	Ala	Thr	Gly	Leu	Ser		
			325					330						335			
Asn	Ile	Phe	Ser	Asp	Lys	Lys	Asp	Gly	Gly	Gln	Tyr	Met	Arg	Cys	Lys		
		340					345						350				
Thr	Gly	Met	Gln	Ser	Ile	Cys	His	Ala	Met	Ser	Lys	Glu	Leu	Val	Pro		
	355					360						365					
Gly	Ser	Val	His	Leu	Asn	Thr	Pro	Val	Ala	Glu	Ile	Glu	Gln	Ser	Ala		
	370					375					380						
Ser	Gly	Cys	Thr	Val	Arg	Ser	Ala	Ser	Gly	Ala	Val	Phe	Arg	Ser	Lys		
385					390					395					400		
Lys	Val	Val	Val	Ser	Leu	Pro	Thr	Thr	Leu	Tyr	Pro	Thr	Leu	Thr	Phe		
			405						410					415			
Ser	Pro	Pro	Leu	Pro	Ala	Glu	Lys	Gln	Ala	Leu	Ala	Glu	Asn	Ser	Ile		
		420					425						430				
Leu	Gly	Tyr	Ser	Lys	Ile	Val	Phe	Val	Trp	Asp	Lys	Pro	Trp	Trp			
	435					440					445						
Arg	Glu	Gln	Gly	Phe	Ser	Gly	Val	Leu	Gln	Ser	Ser	Cys	Asp	Pro	Ile		
	450					455					460						
Ser	Phe	Ala	Arg	Asp	Thr	Ser	Ile	Asp	Val	Asp	Arg	Gln	Trp	Ser	Ile		
465					470					475					480		
Thr	Cys	Phe	Met	Val	Gly	Asp	Pro	Gly	Arg	Lys	Trp	Ser	Gln	Gln	Ser		
			485						490					495			
Lys	Gln	Val	Arg	Gln	Lys	Ser	Val	Trp	Asp	Gln	Leu	Arg	Ala	Ala	Tyr		
		500					505						510				
Glu	Asn	Ala	Gly	Ala	Gln	Val	Pro	Glu	Pro	Ala	Asn	Val	Leu	Glu	Ile		
	515						520					525					
Glu	Trp	Ser	Lys	Gln	Gln	Tyr	Phe	Gln	Gly	Ala	Pro	Ser	Ala	Val	Tyr		
	530					535					540						
Gly	Leu	Asn	Asp	Leu	Ile	Thr	Leu	Gly	Ser	Ala	Leu	Arg	Thr	Pro	Phe		
545					550					555					560		
Lys	Ser	Val	His	Phe	Val	Gly	Thr	Glu	Thr	Ser	Leu	Val	Trp	Lys	Gly		
			565						570					575			
Tyr	Met	Glu	Gly	Ala	Ile	Arg	Ser	Gly	Gln	Arg	Gly	Ala	Ala	Glu	Val		

580 585 590
Val Ala Ser Leu Val Pro Ala Ala
595 600

<210> 24
<211> 3003
<212> DNA
<213> Unknown

<220>
<223> Sequence is barley alpha amylase signal sequence:
esp1 mat: an artificial spacer sequence and
K:trAPAO

<221> sig_peptide
<222> (1)...(72)
<223> Barley alpha amylase signal sequence

<221> misc_feature
<222> (73)...(1575)
<223> esp1 mat

<221> misc_feature
<222> (1576)...(1611)
<223> spacer sequence

<221> misc_feature
<222> (1612)...(3000)
<223> K:trAPAO

<221> CDS
<222> (1)...(3000)

<221> misc_feature
<222> (1612)...(1614)
<223> Extra lysine

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Met Ala Asn Lys His Leu Ser Leu Ser Leu Phe Leu Val Leu Leu Gly
-20 -15 -10
ctc tcc gcc tcc ctc gcc agc ggc gct cct act gtc aag att gat gct 96
Leu Ser Ala Ser Leu Ala Ser Gly Ala Pro Thr Val Lys Ile Asp Ala
-5 1 5
ggg atg gtg gtc ggc acg act act act gtc ccc ggc acc act gcg acc 144
Gly Met Val Val Gly Thr Thr Thr Thr Val Pro Gly Thr Thr Ala Thr
10 15 20
gtc agc gag ttc ttg ggc gtt cct ttt gcc gcc tct ccg aca cga ttt 192
Val Ser Glu Phe Leu Gly Val Pro Phe Ala Ala Ser Pro Thr Arg Phe
25 30 35 40
gcg cct cct act cgt ccc gtg cct tgg tca acg cct ttg caa gcc act 240
Ala Pro Pro Thr Arg Pro Val Pro Trp Ser Thr Pro Leu Gln Ala Thr
45 50 55
gca tat ggt cca gca tgc cct caa caa ttc aat tac ccc gaa gaa ctc 288
Ala Tyr Gly Pro Ala Cys Pro Gln Gln Phe Asn Tyr Pro Glu Glu Leu
60 65 70

cgt gag att acg atg gcc tgg ttc aat aca ccg ccc ccg tca gct ggt	336
Arg Glu Ile Thr Met Ala Trp Phe Asn Thr Pro Pro Ser Ala Gly	
75 80 85	
gaa agt gag gac tgc ctg aac ctc aac atc tac gtc cca gga act gag	384
Glu Ser Glu Asp Cys Leu Asn Leu Asn Ile Tyr Val Pro Gly Thr Glu	
90 95 100	
aac aca aac aaa gcc gtc atg gtt tgg ata tac ggt gga gcg ctg gaa	432
Asn Thr Asn Lys Ala Val Met Val Trp Ile Tyr Gly Gly Ala Leu Glu	
105 110 115 120	
tat ggt tgg aat tca ttc cac ctt tac gac ggg gct agt ttc gca gcc	480
Tyr Gly Trp Asn Ser Phe His Leu Tyr Asp Gly Ala Ser Phe Ala Ala	
125 130 135	
aat cag gat gtc atc gcc gtg acc atc aac tac aga acg aac att ctg	528
Asn Gln Asp Val Ile Ala Val Thr Ile Asn Tyr Arg Thr Asn Ile Leu	
140 145 150	
ggg ttc cct gct gcc cct cag ctt cca ata aca cag cga aat ctg ggg	576
Gly Phe Pro Ala Ala Pro Gln Leu Pro Ile Thr Gln Arg Asn Leu Gly	
155 160 165	
ttc cta gac caa agg ttt gct ttg gat tgg gta cag cgg aac atc gca	624
Phe Leu Asp Gln Arg Phe Ala Leu Asp Trp Val Gln Arg Asn Ile Ala	
170 175 180	
gcc ttt ggc ggt gat cct cga aag gtc aca ata ttt ggg cag agt gcg	672
Ala Phe Gly Gly Asp Pro Arg Lys Val Thr Ile Phe Gly Gln Ser Ala	
185 190 195 200	
ggg ggc aga agt gtc gac gtc ctc ttg acg tct atg cca cac aac cca	720
Gly Gly Arg Ser Val Asp Val Leu Leu Thr Ser Met Pro His Asn Pro	
205 210 215	
ccc ttc cga gca gca atc atg gag tcc ggt gtg gct aac tac aac ttc	768
Pro Phe Arg Ala Ala Ile Met Glu Ser Gly Val Ala Asn Tyr Asn Phe	
220 225 230	
ccc aag gga gat ttg tcc gaa cct tgg aac acc act gtt caa gct ctc	816
Pro Lys Gly Asp Leu Ser Glu Pro Trp Asn Thr Thr Val Gln Ala Leu	
235 240 245	
aac tgt acc acc agt atc gac atc ttg agt tgt atg aga aga gtc gat	864
Asn Cys Thr Thr Ser Ile Asp Ile Leu Ser Cys Met Arg Arg Val Asp	
250 255 260	
ctc gcc act ctg atg aac acg atc gag caa ctc gga ctt ggg ttt gag	912
Leu Ala Thr Leu Met Asn Thr Ile Glu Gln Leu Gly Leu Gly Phe Glu	
265 270 275 280	
tac acg ttg gac aac gta acg gct gtg tac cgt tct gaa acg gct cgc	960
Tyr Thr Leu Asp Asn Val Thr Ala Val Tyr Arg Ser Glu Thr Ala Arg	
285 290 295	
acg act ggt gac att gct cgt gta cct gtt ctc gtc ggg acg gtg gcc	1008
Thr Thr Gly Asp Ile Ala Arg Val Pro Val Leu Val Gly Thr Val Ala	
300 305 310	
aac gac gga ctt ctc ttt gtc ctc ggg gag aat gac acc caa gca tat	1056

Asn Asp Gly Leu Leu Phe Val Leu Gly Glu Asn Asp Thr Gln Ala Tyr	
315 320 325	
ctc gag gag gca atc ccg aat cag ccc gac ctt tac cag act ctc ctt	1104
Leu Glu Glu Ala Ile Pro Asn Gln Pro Asp Leu Tyr Gln Thr Leu Leu	
330 335 340	
gga gca tat ccc att gga tcc cca ggg atc gga tcg cct caa gat cag	1152
Gly Ala Tyr Pro Ile Gly Ser Pro Gly Ile Gly Ser Pro Gln Asp Gln	
345 350 355 360	
att gcc gcc att gag acc gag gta aga ttc cag tgt cct tct gcc atc	1200
Ile Ala Ala Ile Glu Thr Glu Val Arg Phe Gln Cys Pro Ser Ala Ile	
365 370 375	
gtg gct cag gac tcc cgg aat cgg ggt atc cct tct tgg cgc tac tac	1248
Val Ala Gln Asp Ser Arg Asn Arg Gly Ile Pro Ser Trp Arg Tyr Tyr	
380 385 390	
tac aat gcg acc ttt gag aat ctg gag ctt ttc cct ggg tcc gaa gtg	1296
Tyr Asn Ala Thr Phe Glu Asn Leu Glu Leu Phe Pro Gly Ser Glu Val	
395 400 405	
tac cac agc tct gaa gtc ggg atg gtg ttt ggc acg tat cct gtc gca	1344
Tyr His Ser Ser Glu Val Gly Met Val Phe Gly Thr Tyr Pro Val Ala	
410 415 420	
agt gcg acc gcc ttg gag gcc cag acg agc aaa tac atg cag ggt gcc	1392
Ser Ala Thr Ala Leu Glu Ala Gln Thr Ser Lys Tyr Met Gln Gly Ala	
425 430 435 440	
tgg gcg gcc ttt gcc aaa aac ccc atg aat ggg cct ggg tgg aaa caa	1440
Trp Ala Ala Phe Ala Lys Asn Pro Met Asn Gly Pro Gly Trp Lys Gln	
445 450 455	
gtg ccg aat gtc gcg gcg ctt ggc tca cca ggc aaa gcc atc cag gtt	1488
Val Pro Asn Val Ala Ala Leu Gly Ser Pro Gly Lys Ala Ile Gln Val	
460 465 470	
gac gtc tct cca gcg aca ata gac caa cga tgt gcc ttg tac acg cgt	1536
Asp Val Ser Pro Ala Thr Ile Asp Gln Arg Cys Ala Leu Tyr Thr Arg	
475 480 485	
tat tat act gag ttg ggc aca atc gcg ccg agg aca ttt ggc gga ggc	1584
Tyr Tyr Thr Glu Leu Gly Thr Ile Ala Pro Arg Thr Phe Gly Gly Gly	
490 495 500	
agc ggc gga ggc agc ggc gga ggc agc aaa gac aac gtt gcg gac gtg	1632
Ser Gly Gly Gly Ser Gly Gly Gly Ser Lys Asp Asn Val Ala Asp Val	
505 510 515 520	
gta gtg gtg ggc gct ggc ttg agc ggt ttg gag acg gca cgc aaa gtc	1680
Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val	
525 530 535	
cag gcc gcc ggt ctg tcc tgc ctc gtt ctt gag gcg atg gat cgt gta	1728
Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val	
540 545 550	
ggg gga aag act ctg agc gta caa tcg ggt ccc ggc agg acg act atc	1776
Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile	
555 560 565	

aac gac ctc ggc gct gcg tgg atc aat gac agc aac caa agc gaa gta Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val 570 575 580	1824
tcc aga ttg ttt gaa aga ttt cat ttg gag ggc gag ctc cag agg acg Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr 585 590 595 600	1872
act gga aat tca atc cat caa gca caa gac ggt aca acc act aca gct Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala 605 610 615	1920
cct tat ggt gac tcc ttg ctg agc gag gag gtt gca agt gca ctt gcg Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala 620 625 630	1968
gaa ctc ctc ccc gta tgg tct cag ctg atc gaa gag cat agc ctt caa Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln 635 640 645	2016
gac ctc aag gcg agc cct cag gcg aag cgg ctc gac agt gtg agc ttc Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe 650 655 660	2064
gcg cac tac tgt gag aag gaa cta aac ttg cct gct gtt ctc ggc gta Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val 665 670 675 680	2112
gca aac cag atc aca cgc gct ctg ctc ggt gtg gaa gcc cac gag atc Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile 685 690 695	2160
agc atg ctt ttt ctc acc gac tac atc aag agt gcc acc ggt ctc agt Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser 700 705 710	2208
aat att ttc tcg gac aag aaa gac ggc ggg cag tat atg cga tgc aaa Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys 715 720 725	2256
aca ggt atg cag tcg att tgc cat gcc atg tca aag gaa ctt gtt cca Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro 730 735 740	2304
ggc tca gtg cac ctc aac acc ccc gtc gct gaa att gag cag tcg gca Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala 745 750 755 760	2352
tcc ggc tgt aca gta cga tcg gcc tcg ggc gcc gtg ttc cga agc aaa Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys 765 770 775	2400
aag gtg gtg gtt tcg tta ccg aca acc ttg tat ccc acc ttg aca ttt Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe 780 785 790	2448
tca cca cct ctt ccc gcc gag aag caa gca ttg gcg gaa aat tct atc Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile 795 800 805	2496

ctg ggc tac tat agc aag ata gtc ttc gta tgg gac aag ccg tgg tgg	2544
Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp	
810 815 820	
cgc gaa caa ggc ttc tgc ggc gtc ctc caa tgc agc tgt gac ccc atc	2592
Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile	
825 830 835 840	
tca ttt gcc aga gat acc agc atc gac gtc gat cga caa tgg tcc att	2640
Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile	
845 850 855	
acc tgt ttc atg gtc gga gac ccg gga cgg aag tgg tcc caa cag tcc	2688
Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser	
860 865 870	
aag cag gta cga caa aag tct gtc tgg gac caa ctc cgc gca gcc tac	2736
Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr	
875 880 885	
gag aac gcc ggg gcc caa gtc cca gag ccg gcc aac gtg ctc gaa atc	2784
Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile	
890 895 900	
gag tgg tgc aag cag cag tat ttc caa gga gct ccg agc gcc gtc tat	2832
Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr	
905 910 915 920	
ggg ctg aac gat ctc atc aca ctg ggt tgc gcg ctc aga acg ccg ttc	2880
Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe	
925 930 935	
aag agt gtt cat ttc gtt gga acg gag acg tct tta gtt tgg aaa ggg	2928
Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly	
940 945 950	
tat atg gaa ggg gcc ata cga tgc ggt caa cga ggt gct gca gaa gtt	2976
Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val	
955 960 965	
gtg gct agc ctg gtg cca gca gca tag	3003
Val Ala Ser Leu Val Pro Ala Ala	
970 975	

<210> 25
 <211> 1000
 <212> PRT
 <213> Unknown

<220>
 <221> SIGNAL
 <222> (1) ... (24)

<400> 25
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 -5 1 5
 Gly Met Val Val Gly Thr Thr Thr Val Pro Gly Thr Thr Ala Thr
 10 15 20
 Val Ser Glu Phe Leu Gly Val Pro Phe Ala Ala Ser Pro Thr Arg Phe

25	30	35	40
Ala Pro Pro Thr Arg	Pro Val Pro Trp Ser Thr Pro Leu Gln Ala Thr		
	45	50	55
Ala Tyr Gly Pro Ala Cys Pro Gln Gln Phe Asn Tyr Pro Glu Glu Leu			
	60	65	70
Arg Glu Ile Thr Met Ala Trp Phe Asn Thr Pro Pro Pro Ser Ala Gly			
	75	80	85
Glu Ser Glu Asp Cys Leu Asn Leu Asn Ile Tyr Val Pro Gly Thr Glu			
	90	95	100
Asn Thr Asn Lys Ala Val Met Val Trp Ile Tyr Gly Gly Ala Leu Glu			
	105	110	115
Tyr Gly Trp Asn Ser Phe His Leu Tyr Asp Gly Ala Ser Phe Ala Ala			
	125	130	135
Asn Gln Asp Val Ile Ala Val Thr Ile Asn Tyr Arg Thr Asn Ile Leu			
	140	145	150
Gly Phe Pro Ala Ala Pro Gln Leu Pro Ile Thr Gln Arg Asn Leu Gly			
	155	160	165
Phe Leu Asp Gln Arg Phe Ala Leu Asp Trp Val Gln Arg Asn Ile Ala			
	170	175	180
Ala Phe Gly Gly Asp Pro Arg Lys Val Thr Ile Phe Gly Gln Ser Ala			
	185	190	195
Gly Gly Arg Ser Val Asp Val Leu Leu Thr Ser Met Pro His Asn Pro			
	205	210	215
Pro Phe Arg Ala Ala Ile Met Glu Ser Gly Val Ala Asn Tyr Asn Phe			
	220	225	230
Pro Lys Gly Asp Leu Ser Glu Pro Trp Asn Thr Thr Val Gln Ala Leu			
	235	240	245
Asn Cys Thr Thr Ser Ile Asp Ile Leu Ser Cys Met Arg Arg Val Asp			
	250	255	260
Leu Ala Thr Leu Met Asn Thr Ile Glu Gln Leu Gly Leu Gly Phe Glu			
	265	270	275
Tyr Thr Leu Asp Asn Val Thr Ala Val Tyr Arg Ser Glu Thr Ala Arg			
	285	290	295
Thr Thr Gly Asp Ile Ala Arg Val Pro Val Leu Val Gly Thr Val Ala			
	300	305	310
Asn Asp Gly Leu Leu Phe Val Leu Gly Glu Asn Asp Thr Gln Ala Tyr			
	315	320	325
Leu Glu Glu Ala Ile Pro Asn Gln Pro Asp Leu Tyr Gln Thr Leu Leu			
	330	335	340
Gly Ala Tyr Pro Ile Gly Ser Pro Gly Ile Gly Ser Pro Gln Asp Gln			
	345	350	355
Ile Ala Ala Ile Glu Thr Glu Val Arg Phe Gln Cys Pro Ser Ala Ile			
	365	370	375
Val Ala Gln Asp Ser Arg Asn Arg Gly Ile Pro Ser Trp Arg Tyr Tyr			
	380	385	390
Tyr Asn Ala Thr Phe Glu Asn Leu Glu Leu Phe Pro Gly Ser Glu Val			
	395	400	405
Tyr His Ser Ser Glu Val Gly Met Val Phe Gly Thr Tyr Pro Val Ala			
	410	415	420
Ser Ala Thr Ala Leu Glu Ala Gln Thr Ser Lys Tyr Met Gln Gly Ala			
	425	430	435
Trp Ala Ala Phe Ala Lys Asn Pro Met Asn Gly Pro Gly Trp Lys Gln			
	445	450	455
Val Pro Asn Val Ala Ala Leu Gly Ser Pro Gly Lys Ala Ile Gln Val			
	460	465	470
Asp Val Ser Pro Ala Thr Ile Asp Gln Arg Cys Ala Leu Tyr Thr Arg			
	475	480	485
Tyr Tyr Thr Glu Leu Gly Thr Ile Ala Pro Arg Thr Phe Gly Gly Gly			
	490	495	500
Ser Gly Gly Gly Ser Gly Gly Gly Ser Lys Asp Asn Val Ala Asp Val			
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Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val			
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 mature: artificial spacer: and K:trAPAO. For
 plant expression.

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 Leu Ser Ala Ser Leu Ala Ser Gly Thr Asp Phe Pro Val Arg Arg Thr
 -5 1 5
 gat ctg ggc cag gtt cag gga ctg gcc ggg gac gtg atg agc ttt cgc 144
 Asp Leu Gly Gln Val Gln Gly Leu Ala Gly Asp Val Met Ser Phe Arg
 10 15 20
 gga ata ccc tat gca gcg ccg ccg gtg ggc ggg ctg cgt tgg aag ccg 192
 Gly Ile Pro Tyr Ala Ala Pro Pro Val Gly Gly Leu Arg Trp Lys Pro
 25 30 35 40
 ccc caa cac gcc cgg ccc tgg gcg ggc gtt cgc ccc gcc acc caa ttt 240
 Pro Gln His Ala Arg Pro Trp Ala Gly Val Arg Pro Ala Thr Gln Phe
 45 50 55
 ggc tcc gac tgc ttc ggc gcg gcc tat ctt cgc aaa ggc agc ctc gcc 288
 Gly Ser Asp Cys Phe Gly Ala Ala Tyr Leu Arg Lys Gly Ser Leu Ala
 60 65 70
 ccc ggc gtg agc gag gac tgt ctt tac ctc aac gta tgg gcg ccg tca 336
 Pro Gly Val Ser Glu Asp Cys Leu Tyr Leu Asn Val Trp Ala Pro Ser
 75 80 85
 ggc gct aaa ccc gcc cag tac ccc gtc atg gtc tgg gtc tac gcc gcc 384
 Gly Ala Lys Pro Gly Gln Tyr Pro Val Met Val Trp Val Tyr Gly Gly

90	95	100	
ggc ttc gcc ggc ggc acg gcc gcc atg ccc tac tac gac ggc gag gcg Gly Phe Ala Gly Gly Thr Ala Ala Met Pro Tyr Tyr Asp Gly Glu Ala 105 110 115 120			432
ctt gcg cga cag ggc gtc gtc gtg gtg acg ttt aac tat cgg acg aac Leu Ala Arg Gln Gly Val Val Val Val Thr Phe Asn Tyr Arg Thr Asn 125 130 135			480
atc ctg ggc ttt ttc gcc cat cct ggt ctc tcg cgc gag agc ccc acc Ile Leu Gly Phe Phe Ala His Pro Gly Leu Ser Arg Glu Ser Pro Thr 140 145 150			528
gga act tcg ggc aac tac ggc cta ctc gac att ctc gcc gct ctt cgg Gly Thr Ser Gly Asn Tyr Gly Leu Leu Asp Ile Leu Ala Ala Leu Arg 155 160 165			576
tgg gtg cag agc aac gcc cgc gcc ttc gga ggg gac ccc ggc cga gtg Trp Val Gln Ser Asn Ala Arg Ala Phe Gly Gly Asp Pro Gly Arg Val 170 175 180			624
acg gtc ttt ggt gaa tcg gcc gga gcg agc gcg atc gga ctt ctg ctc Thr Val Phe Gly Glu Ser Ala Gly Ala Ser Ala Ile Gly Leu Leu Leu 185 190 195 200			672
acc tcg ccg ctg agc aag ggt ctc ttc cgt ggc gct atc ctc gaa agt Thr Ser Pro Leu Ser Lys Gly Leu Phe Arg Gly Ala Ile Leu Glu Ser 205 210 215			720
cca ggg ctg acg cga ccg ctc gcg acg ctc gcc gac agc gcc gcc tcg Pro Gly Leu Thr Arg Pro Leu Ala Thr Leu Ala Asp Ser Ala Ala Ser 220 225 230			768
ggc gag cgc ctc gac gcc gat ctt tcg cga ctg cgc tcg acc gac cca Gly Glu Arg Leu Asp Ala Asp Leu Ser Arg Leu Arg Ser Thr Asp Pro 235 240 245			816
gcc acc ctg atg gcg cgc gcc gac gcg gcc cgc ccg gca tcg cgg gac Ala Thr Leu Met Ala Arg Ala Asp Ala Ala Arg Pro Ala Ser Arg Asp 250 255 260			864
ctg cgc agg ccg cgt ccg acc gga ccg atc gtc gat ggc cat gtg ctg Leu Arg Arg Pro Arg Thr Gly Pro Ile Val Asp Gly His Val Leu 265 270 275 280			912
ccg cag acc gac agc gcg gcg atc gcg gcg ggg cag ctg gcg ccg gtt Pro Gln Thr Asp Ser Ala Ala Ile Ala Ala Gly Gln Leu Ala Pro Val 285 290 295			960
cgg gtc ctg atc gga acc aat gcc gac gaa ggc cgc gcc ttc ctc ggg Arg Val Leu Ile Gly Thr Asn Ala Asp Glu Gly Arg Ala Phe Leu Gly 300 305 310			1008
cgc gcg ccg atg gag acg cca gcg gac tac caa gcc tat ctg gag gcg Arg Ala Pro Met Glu Thr Pro Ala Asp Tyr Gln Ala Tyr Leu Glu Ala 315 320 325			1056
cag ttt ggc gac caa gcc gcc gcc gtg gcg gcg tgc tat ccc ctc gac Gln Phe Gly Asp Gln Ala Ala Ala Val Ala Ala Cys Tyr Pro Leu Asp 330 335 340			1104

ggc cgg gcc acg ccc aag gaa atg gtc gcg cgc atc ttc ggc gac aat Gly Arg Ala Thr Pro Lys Glu Met Val Ala Arg Ile Phe Gly Asp Asn 345 350 355 360	1152
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aga gcg ccg gct acc cac gga gcc gaa att ccc tac gtt ttc ggg gtg Arg Ala Pro Ala Thr His Gly Ala Glu Ile Pro Tyr Val Phe Gly Val 395 400 405	1296
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acg ccc gcc gac cgt gcg ctg ggc caa ctg atg tcc tcc gcc tgg gtc Thr Pro Ala Asp Arg Ala Leu Gly Gln Leu Met Ser Ser Ala Trp Val 425 430 435 440	1392
cgg ttc gcc aag aat ggc gac ccc gcc ggg gac gcc ctt acc tgg cct Arg Phe Ala Lys Asn Gly Asp Pro Ala Gly Asp Ala Leu Thr Trp Pro 445 450 455	1440
gcc tat tct acg ggc aag tcg acc atg aca ttc ggt ccc gag ggc cgc Ala Tyr Ser Thr Gly Lys Ser Thr Met Thr Phe Gly Pro Glu Gly Arg 460 465 470	1488
gcg gcg gtg gtg tcg ccc gga cct tcc atc ccc cct tgc gcg gat ggc Ala Ala Val Val Ser Pro Gly Pro Ser Ile Pro Pro Cys Ala Asp Gly 475 480 485	1536
gcc aag gcg ggg ggc gga ggc agc ggc gga ggc agc ggc gga ggc agc Ala Lys Ala Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser 490 495 500	1584
aaa gac aac gtt gcg gac gtg gta gtg gtg ggc gct ggc ttg agc ggt Lys Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly 505 510 515 520	1632
ttg gag acg gca cgc aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val 525 530 535	1680
ctt gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tcg Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser 540 545 550	1728
ggt ccc ggc agg acg act atc aac gac ctc ggc gct gcg tgg atc aat Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn 555 560 565	1776
gac agc aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu 570 575 580	1824
gag ggc gag ctc cag agg acg act gga aat tca atc cat caa gca caa Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln	1872

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Asp Gly Thr Thr Thr	Thr Ala Pro Tyr	Gly Asp Ser Leu Leu Ser Glu		
605	610	615		
gag gtt gca agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg			1968	
Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu				
620	625	630		
atc gaa gag cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag			2016	
Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys				
635	640	645		
cgg ctc gac agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac			2064	
Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn				
650	655	660		
ttg cct gct gtt ctc ggc gta gca aac cag atc aca cgc gct ctg ctc			2112	
Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu				
665	670	675	680	
ggt gtg gaa gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc			2160	
Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile				
685	690	695		
aag agt gcc acc ggt ctc agt aat att ttc tcg gac aag aaa gac ggc			2208	
Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly				
700	705	710		
ggg cag tat atg cga tgc aaa aca ggt atg cag tcg att tgc cat gcc			2256	
Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala				
715	720	725		
atg tca aag gaa ctt gtt cca ggc tca gtg cac ctc aac acc ccc gtc			2304	
Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val				
730	735	740		
gct gaa att gag cag tcg gca tcc ggc tgt aca gta cga tcg gcc tcg			2352	
Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser				
745	750	755	760	
ggc gcc gtg ttc cga agc aaa aag gtg gtg gtt tcg tta ccg aca acc			2400	
Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr				
765	770	775		
ttg tat ccc acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa			2448	
Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln				
780	785	790		
gca ttg gcg gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc			2496	
Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe				
795	800	805		
gta tgg gac aag ccg tgg tgg cgc gaa caa ggc ttc tcg gcc gtc ctc			2544	
Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu				
810	815	820		
caa tcg agc tgt gac ccc atc tca ttt gcc aga gat acc agc atc gac			2592	
Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp				
825	830	835	840	

gtc gat cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga	2640
Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly	
845 850 855	
cgg aag tgg tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg	2688
Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp	
860 865 870	
gac caa ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag	2736
Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu	
875 880 885	
ccg gcc aac gtg ctc gaa atc gag tgg tgc aag cag cag tat ttc caa	2784
Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln	
890 895 900	
gga gct ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt	2832
Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly	
905 910 915 920	
tgc gcg ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag	2880
Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu	
925 930 935	
acg tct tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tgc ggt	2928
Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly	
940 945 950	
caa cga ggt gct gca gaa gtt gtg gct agc ctg gtg cca gca gca	2973
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Asp Leu Gly Gln Val Gln Gly Leu Ala Gly Asp Val Met Ser Phe Arg	
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Gly Ile Pro Tyr Ala Ala Pro Pro Val Gly Gly Leu Arg Trp Lys Pro	
25 30 35 40	
Pro Gln His Ala Arg Pro Trp Ala Gly Val Arg Pro Ala Thr Gln Phe	
45 50 55	
Gly Ser Asp Cys Phe Gly Ala Ala Tyr Leu Arg Lys Gly Ser Leu Ala	
60 65 70	
Pro Gly Val Ser Glu Asp Cys Leu Tyr Leu Asn Val Trp Ala Pro Ser	
75 80 85	
Gly Ala Lys Pro Gly Gln Tyr Pro Val Met Val Trp Val Tyr Gly Gly	
90 95 100	
Gly Phe Ala Gly Gly Thr Ala Ala Met Pro Tyr Tyr Asp Gly Glu Ala	
105 110 115 120	

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Ile	Leu	Gly	Phe	Phe	Ala	His	Pro	Gly	Leu	Ser	Arg	Glu	Ser	Pro	Thr	
			140					145					150			
Gly	Thr	Ser	Gly	Asn	Tyr	Gly	Leu	Leu	Asp	Ile	Leu	Ala	Ala	Leu	Arg	
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Trp	Val	Gln	Ser	Asn	Ala	Arg	Ala	Phe	Gly	Gly	Asp	Pro	Gly	Arg	Val	
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Thr	Val	Phe	Gly	Glu	Ser	Ala	Gly	Ala	Ser	Ala	Ile	Gly	Leu	Leu	Leu	
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Thr	Ser	Pro	Leu	Ser	Lys	Gly	Leu	Phe	Arg	Gly	Ala	Ile	Leu	Glu	Ser	
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Pro	Gly	Leu	Thr	Arg	Pro	Leu	Ala	Thr	Leu	Ala	Asp	Ser	Ala	Ala	Ser	
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Gly	Glu	Arg	Leu	Asp	Ala	Asp	Leu	Ser	Arg	Leu	Arg	Ser	Thr	Asp	Pro	
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Leu	Arg	Arg	Pro	Arg	Pro	Thr	Gly	Pro	Ile	Val	Asp	Gly	His	Val	Leu	
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Pro	Gln	Thr	Asp	Ser	Ala	Ala	Ile	Ala	Ala	Gly	Gln	Leu	Ala	Pro	Val	
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Arg	Val	Leu	Ile	Gly	Thr	Asn	Ala	Asp	Glu	Gly	Arg	Ala	Phe	Leu	Gly	
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Arg	Ala	Pro	Met	Glu	Thr	Pro	Ala	Asp	Tyr	Gln	Ala	Tyr	Leu	Glu	Ala	
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Gln	Phe	Gly	Asp	Gln	Ala	Ala	Val	Ala	Ala	Cys	Tyr	Pro	Leu	Asp		
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Gln	Phe	Asn	Arg	Gly	Val	Ser	Ala	Phe	Ser	Glu	Ala	Leu	Val	Arg	Gln	
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		380						385					390			
Arg	Ala	Pro	Ala	Thr	His	Gly	Ala	Glu	Ile	Pro	Tyr	Val	Phe	Gly	Val	
	395						400					405				
Phe	Lys	Leu	Asp	Glu	Leu	Gly	Leu	Phe	Asp	Trp	Pro	Pro	Glu	Gly	Pro	
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Thr	Pro	Ala	Asp	Arg	Ala	Leu	Gly	Gln	Leu	Met	Ser	Ser	Ala	Trp	Val	
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Arg	Phe	Ala	Lys	Asn	Gly	Asp	Pro	Ala	Gly	Asp	Ala	Leu	Thr	Trp	Pro	
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Ala	Tyr	Ser	Thr	Gly	Lys	Ser	Thr	Met	Thr	Phe	Gly	Pro	Glu	Gly	Arg	
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Ala	Ala	Val	Val	Ser	Pro	Gly	Pro	Ser	Ile	Pro	Pro	Cys	Ala	Asp	Gly	
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Ala	Lys	Ala	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Ser	
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Lys	Asp	Asn	Val	Ala	Asp	Val	Val	Val	Val	Gly	Ala	Gly	Leu	Ser	Gly	
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Leu	Glu	Thr	Ala	Arg	Lys	Val	Gln	Ala	Ala	Gly	Leu	Ser	Cys	Leu	Val	
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Leu	Glu	Ala	Met	Asp	Arg	Val	Gly	Gly	Lys	Thr	Leu	Ser	Val	Gln	Ser	
		540						545					550			
Gly	Pro	Gly	Arg	Thr	Thr	Ile	Asn	Asp	Leu	Gly	Ala	Ala	Trp	Ile	Asn	
	555						560					565				
Asp	Ser	Asn	Gln	Ser	Glu	Val	Ser	Arg	Leu	Phe	Glu	Arg	Phe	His	Leu	
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Glu	Gly	Glu	Leu	Gln	Arg	Thr	Thr	Gly	Asn	Ser	Ile	His	Gln	Ala	Gln	
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Asp	Gly	Thr	Thr	Thr	Ala	Pro	Tyr	Gly	Asp	Ser	Leu	Leu	Ser	Glu		
			605					610						615		

Glu	Val	Ala	Ser	Ala	Leu	Ala	Glu	Leu	Leu	Pro	Val	Trp	Ser	Gln	Leu
			620					625					630		
Ile	Glu	Glu	His	Ser	Leu	Gln	Asp	Leu	Lys	Ala	Ser	Pro	Gln	Ala	Lys
		635					640					645			
Arg	Leu	Asp	Ser	Val	Ser	Phe	Ala	His	Tyr	Cys	Glu	Lys	Glu	Leu	Asn
	650					655					660				
Leu	Pro	Ala	Val	Leu	Gly	Val	Ala	Asn	Gln	Ile	Thr	Arg	Ala	Leu	Leu
665					670					675					680
Gly	Val	Glu	Ala	His	Glu	Ile	Ser	Met	Leu	Phe	Leu	Thr	Asp	Tyr	Ile
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Gly	Gln	Tyr	Met	Arg	Cys	Lys	Thr	Gly	Met	Gln	Ser	Ile	Cys	His	Ala
	715						720					725			
Met	Ser	Lys	Glu	Leu	Val	Pro	Gly	Ser	Val	His	Leu	Asn	Thr	Pro	Val
	730					735					740				
Ala	Glu	Ile	Glu	Gln	Ser	Ala	Ser	Gly	Cys	Thr	Val	Arg	Ser	Ala	Ser
745					750					755					760
Gly	Ala	Val	Phe	Arg	Ser	Lys	Lys	Val	Val	Val	Ser	Leu	Pro	Thr	Thr
			765					770					775		
Leu	Tyr	Pro	Thr	Leu	Thr	Phe	Ser	Pro	Pro	Leu	Pro	Ala	Glu	Lys	Gln
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Ala	Leu	Ala	Glu	Asn	Ser	Ile	Leu	Gly	Tyr	Tyr	Ser	Lys	Ile	Val	Phe
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Val	Trp	Asp	Lys	Pro	Trp	Trp	Arg	Glu	Gln	Gly	Phe	Ser	Gly	Val	Leu
	810				815					820					
Gln	Ser	Ser	Cys	Asp	Pro	Ile	Ser	Phe	Ala	Arg	Asp	Thr	Ser	Ile	Asp
825				830						835					840
Val	Asp	Arg	Gln	Trp	Ser	Ile	Thr	Cys	Phe	Met	Val	Gly	Asp	Pro	Gly
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Arg	Lys	Trp	Ser	Gln	Gln	Ser	Lys	Gln	Val	Arg	Gln	Lys	Ser	Val	Trp
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Pro	Ala	Asn	Val	Leu	Glu	Ile	Glu	Trp	Ser	Lys	Gln	Gln	Tyr	Phe	Gln
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Gly	Ala	Pro	Ser	Ala	Val	Tyr	Gly	Leu	Asn	Asp	Leu	Ile	Thr	Leu	Gly
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Ser	Ala	Leu	Arg	Thr	Pro	Phe	Lys	Ser	Val	His	Phe	Val	Gly	Thr	Glu
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Thr	Ser	Leu	Val	Trp	Lys	Gly	Tyr	Met	Glu	Gly	Ala	Ile	Arg	Ser	Gly
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 2227-3615, K:trAPAO, 3616-3618, stop codon. For
 bacterial expression.

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<223> gst + polylinker

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<223> Extra lysine

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Thr	Arg	Leu	Leu	Leu	Glu	Tyr	Leu	Glu	Glu	Lys	Tyr	Glu	Glu	His	Leu	
			20					25					30			

tat	gag	cgc	gat	gaa	ggt	gat	aaa	tgg	cga	aac	aaa	aag	ttt	gaa	ttg	144
Tyr	Glu	Arg	Asp	Glu	Gly	Asp	Lys	Trp	Arg	Asn	Lys	Lys	Phe	Glu	Leu	
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Gly	Leu	Glu	Phe	Pro	Asn	Leu	Pro	Tyr	Tyr	Ile	Asp	Gly	Asp	Val	Lys	
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Leu	Thr	Gln	Ser	Met	Ala	Ile	Ile	Arg	Tyr	Ile	Ala	Asp	Lys	His	Asn	
	65				70					75					80	

atg	ttg	ggt	ggt	tgt	cca	aaa	gag	cgt	gca	gag	att	tca	atg	ctt	gaa	288
Met	Leu	Gly	Gly	Cys	Pro	Lys	Glu	Arg	Ala	Glu	Ile	Ser	Met	Leu	Glu	
				85					90					95		

gga	gcg	gtt	ttg	gat	att	aga	tac	ggt	gtt	tcg	aga	att	gca	tat	agt	336
Gly	Ala	Val	Leu	Asp	Ile	Arg	Tyr	Gly	Val	Ser	Arg	Ile	Ala	Tyr	Ser	
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aaa	gac	ttt	gaa	act	ctc	aaa	gtt	gat	ttt	ctt	agc	aag	cta	cct	gaa	384
Lys	Asp	Phe	Glu	Thr	Leu	Lys	Val	Asp	Phe	Leu	Ser	Lys	Leu	Pro	Glu	
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atg	ctg	aaa	atg	ttc	gaa	gat	cgt	tta	tgt	cat	aaa	aca	tat	tta	aat	432
Met	Leu	Lys	Met	Phe	Glu	Asp	Arg	Leu	Cys	His	Lys	Thr	Tyr	Leu	Asn	
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Gly	Asp	His	Val	Thr	His	Pro	Asp	Phe	Met	Leu	Tyr	Asp	Ala	Leu	Asp	
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Val	Val	Leu	Tyr	Met	Asp	Pro	Met	Cys	Leu	Asp	Ala	Phe	Pro	Lys	Leu	
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Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr	
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ttg aaa tcc agc aag tat ata gca tgg cct ttg cag ggc tgg caa gcc	624
Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala	
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acg ttt ggt ggt ggc gac cat cct cca aaa tcg gat ctg gtt ccg cgt	672
Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg	
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Gly Ser Pro Glu Phe Ala Pro Thr Val Lys Ile Asp Ala Gly Met Val	
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Val Gly Thr Thr Thr Val Pro Gly Thr Thr Ala Thr Val Ser Glu	
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Phe Leu Gly Val Pro Phe Ala Ala Ser Pro Thr Arg Phe Ala Pro Pro	
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Val Ile Ala Val Thr Ile Asn Tyr Arg Thr Asn Ile Leu Gly Phe Pro	
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Ala Ala Pro Gln Leu Pro Ile Thr Gln Arg Asn Leu Gly Phe Leu Asp	
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Gln Arg Phe Ala Leu Asp Trp Val Gln Arg Asn Ile Ala Ala Phe Gly	
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Thr	Ser	Ile	Asp	Ile	Leu	Ser	Cys	Met	Arg	Arg	Val	Asp	Leu	Ala	Thr		
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Asp	Asn	Val	Thr	Ala	Val	Tyr	Arg	Ser	Glu	Thr	Ala	Arg	Thr	Thr	Gly		
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Asp	Ile	Ala	Arg	Val	Pro	Val	Leu	Val	Gly	Thr	Val	Ala	Asn	Asp	Gly		
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ctt	ctc	ttt	gtc	ctc	ggg	gag	aat	gac	acc	caa	gca	tat	ctc	gag	gag	1680	
Leu	Leu	Phe	Val	Leu	Gly	Glu	Asn	Asp	Thr	Gln	Ala	Tyr	Leu	Glu	Glu		
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Ile	Glu	Thr	Glu	Val	Arg	Phe	Gln	Cys	Pro	Ser	Ala	Ile	Val	Ala	Gln		
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Thr	Phe	Glu	Asn	Leu	Glu	Phe	Pro	Gly	Ser	Glu	Val	Tyr	His	Ser			
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Ser	Glu	Val	Gly	Met	Val	Phe	Gly	Thr	Tyr	Pro	Val	Ala	Ser	Ala	Thr		
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tca atc cat caa gca caa gac ggt aca acc act aca gct cct tat ggt Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala Pro Tyr Gly 835 840 845	2544
gac tcc ttg ctg agc gag gag gtt gca agt gca ctt gcg gaa ctc ctc Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu Leu Leu 850 855 860	2592
ccc gta tgg tct cag ctg atc gaa gag cat agc ctt caa gac ctc aag Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln Asp Leu Lys 865 870 875 880	2640
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Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser Met Leu	
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Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro Gly Ser Val	
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His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys	
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Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp Arg Glu Gln	
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Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala	
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Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser Lys Gln Val	
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 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn
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 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu
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 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu
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 Gly Leu Glu Phe Pro Asn Leu Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys
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Leu	Lys	Ser	Ser	Lys	Tyr	Ile	Ala	Trp	Pro	Leu	Gln	Gly	Trp	Gln	Ala	
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Thr	Phe	Gly	Gly	Gly	Asp	His	Pro	Pro	Lys	Ser	Asp	Leu	Val	Pro	Arg	
	210					215					220					
gga	tcc	ccg	gaa	ttc	acg	gat	ttt	ccg	gtc	cgc	agg	acc	gat	ctg	ggc	720
Gly	Ser	Pro	Glu	Phe	Thr	Asp	Phe	Pro	Val	Arg	Arg	Thr	Asp	Leu	Gly	
225					230					235				240		
cag	ggt	cag	gga	ctg	gcc	ggg	gac	gtg	atg	agc	ttt	cgc	gga	ata	ccc	768
Gln	Val	Gln	Gly	Leu	Ala	Gly	Asp	Val	Met	Ser	Phe	Arg	Gly	Ile	Pro	
				245					250					255		
tat	gca	gcg	ccg	ccg	gtg	ggc	ggg	ctg	cgt	tgg	aag	ccg	ccc	caa	cac	816
Tyr	Ala	Ala	Pro	Pro	Val	Gly	Gly	Leu	Arg	Trp	Lys	Pro	Pro	Gln	His	
			260					265					270			
gcc	cgg	ccc	tgg	gcg	ggc	ggt	cgc	ccc	gcc	acc	caa	ttt	ggc	tcc	gac	864
Ala	Arg	Pro	Trp	Ala	Gly	Val	Arg	Pro	Ala	Thr	Gln	Phe	Gly	Ser	Asp	
		275					280					285				
tgc	ttc	ggc	gcg	gcc	tat	ctt	cgc	aaa	ggc	agc	ctc	gcc	ccc	ggc	gtg	912
Cys	Phe	Gly	Ala	Ala	Tyr	Leu	Arg	Lys	Gly	Ser	Leu	Ala	Pro	Gly	Val	
	290					295					300					
agc	gag	gac	tgt	ctt	tac	ctc	aac	gta	tgg	gcg	ccg	tca	ggc	gct	aaa	960
Ser	Glu	Asp	Cys	Leu	Tyr	Leu	Asn	Val	Trp	Ala	Pro	Ser	Gly	Ala	Lys	
305					310					315				320		
ccc	ggc	cag	tac	ccc	gtc	atg	gtc	tgg	gtc	tac	ggc	ggc	ggc	ttc	gcc	1008
Pro	Gly	Gln	Tyr	Pro	Val	Met	Val	Trp	Val	Tyr	Gly	Gly	Gly	Phe	Ala	
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ggc	ggc	acg	gcc	gcc	atg	ccc	tac	tac	gac	ggc	gag	gcg	ctt	gcg	cga	1056
Gly	Gly	Thr	Ala	Ala	Met	Pro	Tyr	Tyr	Asp	Gly	Glu	Ala	Leu	Ala	Arg	
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cag	ggc	gtc	gtc	gtg	gtg	acg	ttt	aac	tat	cgg	acg	aac	atc	ctg	ggc	1104
Gln	Gly	Val	Val	Val	Val	Thr	Phe	Asn	Tyr	Arg	Thr	Asn	Ile	Leu	Gly	
		355					360					365				
ttt	ttc	gcc	cat	cct	ggt	ctc	tcg	cgc	gag	agc	ccc	acc	gga	act	tcg	1152
Phe	Phe	Ala	His	Pro	Gly	Leu	Ser	Arg	Glu	Ser	Pro	Thr	Gly	Thr	Ser	
	370					375					380					
ggc	aac	tac	ggc	cta	ctc	gac	att	ctc	gcc	gct	ctt	cgg	tgg	gtg	cag	1200
Gly	Asn	Tyr	Gly	Leu	Leu	Asp	Ile	Leu	Ala	Ala	Leu	Arg	Trp	Val	Gln	
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ggt gaa tcg gcc gga gcg agc gcg atc gga ctt ctg ctc acc tcg ccg Gly Glu Ser Ala Gly Ala Ser Ala Ile Gly Leu Leu Leu Thr Ser Pro 420 425 430	1296
ctg agc aag ggt ctc ttc cgt ggc gct atc ctc gaa agt cca ggg ctg Leu Ser Lys Gly Leu Phe Arg Gly Ala Ile Leu Glu Ser Pro Gly Leu 435 440 445	1344
acg cga ccg ctc gcg acg ctc gcc gac agc gcc gcc tcg ggc gag cgc Thr Arg Pro Leu Ala Thr Leu Ala Asp Ser Ala Ala Ser Gly Glu Arg 450 455 460	1392
ctc gac gcc gat ctt tcg cga ctg cgc tcg acc gac cca gcc acc ctg Leu Asp Ala Asp Leu Ser Arg Leu Arg Ser Thr Asp Pro Ala Thr Leu 465 470 475 480	1440
atg gcg cgc gcc gac gcg gcc cgc ccg gca tcg cgg gac ctg cgc agg Met Ala Arg Ala Asp Ala Ala Arg Pro Ala Ser Arg Asp Leu Arg Arg 485 490 495	1488
ccg cgt ccg acc gga ccg atc gtc gat ggc cat gtg ctg ccg cag acc Pro Arg Pro Thr Gly Pro Ile Val Asp Gly His Val Leu Pro Gln Thr 500 505 510	1536
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Asp Glu Leu Gly Leu Phe Asp Trp Pro Pro Glu Gly Pro Thr Pro Ala	
645	650 655
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Asp Arg Ala Leu Gly Gln Leu Met Ser Ser Ala Trp Val Arg Phe Ala	
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Lys Asn Gly Asp Pro Ala Gly Asp Ala Leu Thr Trp Pro Ala Tyr Ser	
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Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr	
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Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn	
785 790 795 800	
caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg gag ggc gag	2448
Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu	
805 810 815	
ctc cag agg acg act gga aat tca atc cat caa gca caa gac ggt aca	2496
Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr	
820 825 830	
acc act aca gct cct tat ggt gac tcc ttg ctg agc gag gag gtt gca	2544
Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala	
835 840 845	
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Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu	
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His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp	
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Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala	
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gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc gta tgg gac Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp 1025 1030 1035 1040	3120
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Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu	
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Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu	
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Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys	
50 55 60	
Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn	
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Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser	
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Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu	
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130 135 140	
Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp	
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Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu	
165 170 175	
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Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala	
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Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg	
210 215 220	
Gly Ser Pro Glu Phe Thr Asp Phe Pro Val Arg Arg Thr Asp Leu Gly	
225 230 235 240	
Gln Val Gln Gly Leu Ala Gly Asp Val Met Ser Phe Arg Gly Ile Pro	
245 250 255	
Tyr Ala Ala Pro Pro Val Gly Gly Leu Arg Trp Lys Pro Pro Gln His	
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Ala Arg Pro Trp Ala Gly Val Arg Pro Ala Thr Gln Phe Gly Ser Asp	
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Cys Phe Gly Ala Ala Tyr Leu Arg Lys Gly Ser Leu Ala Pro Gly Val	
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Ser Glu Asp Cys Leu Tyr Leu Asn Val Trp Ala Pro Ser Gly Ala Lys	
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Pro Gly Gln Tyr Pro Val Met Val Trp Val Tyr Gly Gly Gly Phe Ala
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 Gly Gly Thr Ala Ala Met Pro Tyr Tyr Asp Gly Glu Ala Leu Ala Arg
 340 345 350
 Gln Gly Val Val Val Thr Phe Asn Tyr Arg Thr Asn Ile Leu Gly
 355 360 365
 Phe Phe Ala His Pro Gly Leu Ser Arg Glu Ser Pro Thr Gly Thr Ser
 370 375 380
 Gly Asn Tyr Gly Leu Leu Asp Ile Leu Ala Ala Leu Arg Trp Val Gln
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 Ser Asn Ala Arg Ala Phe Gly Gly Asp Pro Gly Arg Val Thr Val Phe
 405 410 415
 Gly Glu Ser Ala Gly Ala Ser Ala Ile Gly Leu Leu Leu Thr Ser Pro
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 Leu Ser Lys Gly Leu Phe Arg Gly Ala Ile Leu Glu Ser Pro Gly Leu
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 Thr Arg Pro Leu Ala Thr Leu Ala Asp Ser Ala Ala Ser Gly Glu Arg
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 Met Ala Arg Ala Asp Ala Ala Arg Pro Ala Ser Arg Asp Leu Arg Arg
 485 490 495
 Pro Arg Pro Thr Gly Pro Ile Val Asp Gly His Val Leu Pro Gln Thr
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 Asp Ser Ala Ala Ile Ala Ala Gly Gln Leu Ala Pro Val Arg Val Leu
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 Asp Arg Ala Leu Gly Gln Leu Met Ser Ser Ala Trp Val Arg Phe Ala
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 Thr Gly Lys Ser Thr Met Thr Phe Gly Pro Glu Gly Arg Ala Ala Val
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 785 790 795 800
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 Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala
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 His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp
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 Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala
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 950 955 960
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 980 985 990
 Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro
 995 1000 1005
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 Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp
 1075 1080 1085
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 1125 1130 1135
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Ala Gly Tyr Ser His Val Gly Val Gly Pro Asp Gly Gly Arg Tyr Val	
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Thr Ile Ala Gly Gln Ile Gly Gln Asp Ala Ser Gly Val Thr Asp Pro	
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gcc tac gag aaa cag gtt gcc caa gca ttc gcc aat ctg cga gct tgc	192
Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys	
50 55 60	
ctt gct gca gtt gga gcc act tca aac gac gtc acc aag ctc aat tac	240
Leu Ala Ala Val Gly Ala Thr Ser Asn Asp Val Thr Lys Leu Asn Tyr	
65 70 75 80	
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Tyr Ile Val Asp Tyr Ala Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly	
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Leu Lys Ala Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val	
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cca gtg tcg gcc ttg tct tca cct gaa tac ctc ttt gag gtt gat gcc	384
Pro Val Ser Ala Leu Ser Ser Pro Glu Tyr Leu Phe Glu Val Asp Ala	
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Thr Ala Leu Val Pro Gly His Thr Thr Pro Asp Asn Val Ala Asp Val	
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Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val	
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Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val	
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Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr	
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Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala	

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Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val			
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Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile			
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Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser			
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Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys			
340	345	350	
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Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro			
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Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala			
370	375	380	
tcc ggc tgt aca gta cga tcg gcc tcg ggc gcc gtg ttc cga agc aaa			1200
Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys			
385	390	395	400
aag gtg gtg gtt tcg tta ccg aca acc ttg tat ccc acc ttg aca ttt			1248
Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe			
405	410	415	
tca cca cct ctt ccc gcc gag aag caa gca ttg gcg gaa aat tct atc			1296
Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile			
420	425	430	
ctg ggc tac tat agc aag ata gtc ttc gta tgg gac aag ccg tgg tgg			1344
Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp			
435	440	445	
cgc gaa caa ggc ttc tcg ggc gtc ctc caa tcg agc tgt gac ccc atc			1392
Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile			
450	455	460	
tca ttt gcc aga gat acc agc atc gac gtc gat cga caa tgg tcc att			1440
Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile			
465	470	475	480
acc tgt ttc atg gtc gga gac ccg gga cgg aag tgg tcc caa cag tcc			1488
Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser			
485	490	495	

aag cag gta cga caa aag tct gtc tgg gac caa ctc cgc gca gcc tac	1536
Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr	
500 505 510	
gag aac gcc ggg gcc caa gtc cca gag ccg gcc aac gtg ctc gaa atc	1584
Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile	
515 520 525	
gag tgg tcg aag cag cag tat ttc caa gga gct ccg agc gcc gtc tat	1632
Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr	
530 535 540	
ggg ctg aac gat ctc atc aca ctg ggt tcg gcg ctc aga acg ccg ttc	1680
Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe	
545 550 555 560	
aag agt gtt cat ttc gtt gga acg gag acg tct tta gtt tgg aaa ggg	1728
Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly	
565 570 575	
tat atg gaa ggg gcc ata cga tcg ggt caa cga ggt gct gca gaa gtt	1776
Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val	
580 585 590	
gtg gct agc ctg gtg cca gca gca tag	1803
Val Ala Ser Leu Val Pro Ala Ala *	
595 600	

<210> 33
 <211> 600
 <212> PRT
 <213> Unknown

<400> 33

Met Ala Leu Ala Pro Ser Tyr Ile Asn Pro Pro Asn Val Ala Ser Pro	
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Ala Gly Tyr Ser His Val Gly Val Gly Pro Asp Gly Gly Arg Tyr Val	
20 25 30	
Thr Ile Ala Gly Gln Ile Gly Gln Asp Ala Ser Gly Val Thr Asp Pro	
35 40 45	
Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys	
50 55 60	
Leu Ala Ala Val Gly Ala Thr Ser Asn Asp Val Thr Lys Leu Asn Tyr	
65 70 75 80	
Tyr Ile Val Asp Tyr Ala Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly	
85 90 95	
Leu Lys Ala Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val	
100 105 110	
Pro Val Ser Ala Leu Ser Ser Pro Glu Tyr Leu Phe Glu Val Asp Ala	
115 120 125	
Thr Ala Leu Val Pro Gly His Thr Thr Pro Asp Asn Val Ala Asp Val	
130 135 140	
Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val	
145 150 155 160	
Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val	
165 170 175	
Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile	
180 185 190	
Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ala Glu Val	
195 200 205	
Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr	

210		215		220
Thr Gly Asn Ser Ile His	Gln Ala Gln Asp Gly	Thr Thr Thr Thr Ala		
225	230	235		240
Pro Tyr Gly Asp Ser Leu	Leu Ser Glu Glu Val	Ala Ser Ala Leu Ala		
	245	250		255
Glu Leu Leu Pro Val Trp	Ser Gln Leu Ile Glu	Glu Glu His Ser Leu Gln		
	260	265		270
Asp Leu Lys Ala Ser Pro	Gln Ala Lys Arg Leu	Asp Ser Val Ser Phe		
	275	280		285
Ala His Tyr Cys Glu Lys	Glu Leu Asn Leu Pro	Ala Val Leu Gly Val		
	290	295		300
Ala Asn Gln Ile Thr Arg	Ala Leu Leu Gly Val	Glu Ala His Glu Ile		
305	310	315		320
Ser Met Leu Phe Leu Thr	Asp Tyr Ile Lys Ser	Ala Thr Gly Leu Ser		
	325	330		335
Asn Ile Phe Ser Asp Lys	Lys Asp Gly Gly Gln	Tyr Met Arg Cys Lys		
	340	345		350
Thr Gly Met Gln Ser Ile	Cys His Ala Met Ser	Lys Glu Leu Val Pro		
	355	360		365
Gly Ser Val His Leu Asn	Thr Pro Val Ala Glu	Ile Glu Gln Ser Ala		
	370	375		380
Ser Gly Cys Thr Val Arg	Ser Ala Ser Gly Ala	Val Phe Arg Ser Lys		
385	390	395		400
Lys Val Val Val Ser Leu	Pro Thr Thr Leu Tyr	Pro Thr Leu Thr Phe		
	405	410		415
Ser Pro Pro Leu Pro Ala	Glu Lys Gln Ala Leu	Ala Glu Asn Ser Ile		
	420	425		430
Leu Gly Tyr Ser Lys Ile	Val Phe Val Trp Asp	Lys Pro Trp Trp		
	435	440		445
Arg Glu Gln Gly Phe Ser	Gly Val Leu Gln Ser	Ser Ser Cys Asp Pro Ile		
	450	455		460
Ser Phe Ala Arg Asp Thr	Ser Ile Asp Val Asp	Arg Gln Trp Ser Ile		
465	470	475		480
Thr Cys Phe Met Val Gly	Asp Pro Gly Arg Lys	Trp Ser Gln Gln Ser		
	485	490		495
Lys Gln Val Arg Gln Lys	Ser Val Trp Asp Gln	Leu Arg Ala Ala Tyr		
	500	505		510
Glu Asn Ala Gly Ala Gln	Val Pro Glu Pro Ala	Asn Val Leu Glu Ile		
	515	520		525
Glu Trp Ser Lys Gln Gln	Tyr Phe Gln Gly Ala	Pro Ser Ala Val Tyr		
	530	535		540
Gly Leu Asn Asp Leu Ile	Thr Leu Gly Ser Ala	Leu Arg Thr Pro Phe		
545	550	555		560
Lys Ser Val His Phe Val	Gly Thr Glu Thr Ser	Leu Val Trp Lys Gly		
	565	570		575
Tyr Met Glu Gly Ala Ile	Arg Ser Gly Gln Arg	Gly Ala Ala Glu Val		
	580	585		590
Val Ala Ser Leu Val Pro	Ala Ala			
	595	600		

<210> 34
 <211> 37
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> 37-mer oligonucleotide

<400> 34
 ggggaattca tggcacttgc accgagctac atcaatc

<210> 35

<211> 1929
 <212> DNA
 <213> *Exophiala spinifera*

<220>
 <221> intron
 <222> (739)...(811)

<221> intron
 <222> (1134)...(1186)

<400> 35

atggcacttg	caccgagcta	catcaatccc	ccaaacgtcg	cctccccagc	agggtattcc	60
cacatcggcg	taggccccaa	cgaagcgagg	tatgtgacaa	tagctggaca	gattggacaa	120
gacgcttttg	gcgtgacaga	cccagcctac	gagaaacagg	ttgccaagc	attcgccaat	180
ctgcgagctt	gccttgctgc	agttggagcc	tcttcaaacg	acgtcaccaa	gctcaattac	240
tacatcgtcg	actacgcccc	gagcaaaactc	accgcaattg	gagatgggct	gaagtctacc	300
tttgcccttg	acaggctccc	tccttgcaag	ctggtgccag	taccggcctt	ggcttcacct	360
gaatacctct	ttgaggttga	tgccaacggcg	ctggtgccag	gacactcgac	cccagacaac	420
gttgcgagcg	tggtagtggg	gggcgctggc	ttgagcggtt	tggagacggc	acgcaaagtc	480
caggccggcg	gtctgtcttg	cctcgttctt	gaggcgatgg	atcgtgtagg	gggaaagact	540
ctgagcgtac	aatcgggtcc	cggcaggacg	actatcaacg	acctcggcgc	tgctgggatc	600
aatgacagca	accaaagcga	agtatccaga	ttgtttgaaa	gatttcattt	ggaggcgag	660
ctccagagga	cgaccggaaa	ttcaatccat	caagcacaag	acggtacaac	cactacagct	720
ccttatgggtg	actccccggg	aagcacaaatc	ccactttgtg	atgagacctc	tgctgagtgt	780
agaatacagt	cactgactcc	acttcgtcca	gctgagcgag	gagggttcaa	gtgcacttgc	840
ggaactcctc	cccgtatggg	ctcagctgat	cgaagagtat	agccttgaag	accccaaggc	900
gagccctcag	gcgaagcggc	tcgacagtgt	gagcttcgcg	cactactgtg	agaaggacct	960
aaacttgctt	gctgttctca	gcgtggcaaa	ccagatcaca	cgcgctctgc	tcgggtgtgga	1020
agcccacgag	atcagcatgc	tttttctcac	cgactacatc	aagagtgcc	ccggtctcag	1080
taatattgtc	tcggacaaga	aagacggcgg	gcagtatatg	cgatgcaaaa	cagggtgcgtg	1140
cggtgtcctc	tcaggtaggg	gactcgtttc	ttagtggtea	ttccagggtat	gcagtcgatt	1200
tgccatgcc	tgtcaaagga	acttgttcca	ggctcagtg	acctcaacac	ccccgtcgct	1260
ggaattgagc	agtcggcgctc	cggctgtata	gtacgatcgg	cctcgggcgc	cgtgttccga	1320
agcaaaaagg	tggtgggttc	gttaccgaca	acattgtatc	ccaccttgac	attttcacca	1380
cctcttcccg	ccgagaagca	agcattggcg	gaaaaatcta	tcctcggcta	ctatagcaag	1440
atagtcttcg	tatgggacaa	cccgtgggtg	cgcaacaag	gcttctcggg	cgctcctcaa	1500
tcgagctgtg	accccatctc	atttgccaga	gataccagca	tcgaagtcga	tcggcaatgg	1560
tccattacct	gtttcatggg	cggagaccgc	ggacggaagt	ggtcccaaca	gtccaagcag	1620
gtacgacaaa	agtctgtctg	ggaccaactc	cgcgagcct	acgagaacgc	cggggcccaa	1680
gtcccagagc	cggccaacgt	gctcgaaatc	gagtggctga	agcagcagta	tttccaagga	1740
gctccgagcg	ccgtctatgg	gctgaacgat	ctcatcacac	tgggttcggc	gctcagaacg	1800
ccgttcaagt	gtgttcattt	cgttgaacg	gagacgtctt	tagtttggaa	agggtatatg	1860
gaaggggcca	tacgatcggg	tcaacgaggt	gctgcagaag	ttgtggctag	cctggtgcc	1920
gcagcatag						1929

<210> 36
 <211> 600
 <212> PRT
 <213> *Exophiala spinifera*

<400> 36

Met	Ala	Leu	Ala	Pro	Ser	Tyr	Ile	Asn	Pro	Pro	Asn	Val	Ala	Ser	Pro
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Ala	Gly	Tyr	Ser	His	Ile	Gly	Val	Gly	Pro	Asn	Glu	Ala	Arg	Tyr	Val
			20					25					30		
Thr	Ile	Ala	Gly	Gln	Ile	Gly	Gln	Asp	Ala	Leu	Gly	Val	Thr	Asp	Pro
		35					40					45			
Ala	Tyr	Glu	Lys	Gln	Val	Ala	Gln	Ala	Phe	Ala	Asn	Leu	Arg	Ala	Cys
	50					55					60				
Leu	Ala	Ala	Val	Gly	Ala	Ser	Ser	Asn	Asp	Val	Thr	Lys	Leu	Asn	Tyr
65					70					75				80	

Tyr Ile Val Asp Tyr Ala Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly
 85 90 95
 Leu Lys Ser Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val
 100 105 110
 Pro Val Pro Ala Leu Ala Ser Pro Glu Tyr Leu Phe Glu Val Asp Ala
 115 120 125
 Thr Ala Leu Val Pro Gly His Ser Thr Pro Asp Asn Val Ala Asp Val
 130 135 140
 Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val
 145 150 155 160
 Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val
 165 170 175
 Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile
 180 185 190
 Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val
 195 200 205
 Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr
 210 215 220
 Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala
 225 230 235 240
 Pro Tyr Gly Asp Ser Pro Leu Ser Glu Glu Val Ala Ser Ala Leu Ala
 245 250 255
 Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu Tyr Ser Leu Glu
 260 265 270
 Asp Pro Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe
 275 280 285
 Ala His Tyr Cys Glu Lys Asp Leu Asn Leu Pro Ala Val Leu Ser Val
 290 295 300
 Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile
 305 310 315 320
 Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser
 325 330 335
 Asn Ile Val Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys
 340 345 350
 Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro
 355 360 365
 Gly Ser Val His Leu Asn Thr Pro Val Ala Gly Ile Glu Gln Ser Ala
 370 375 380
 Ser Gly Cys Ile Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys
 385 390 395 400
 Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe
 405 410 415
 Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Lys Ser Ile
 420 425 430
 Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Asn Pro Trp Trp
 435 440 445
 Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile
 450 455 460
 Ser Phe Ala Arg Asp Thr Ser Ile Glu Val Asp Arg Gln Trp Ser Ile
 465 470 475 480
 Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser
 485 490 495
 Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr
 500 505 510
 Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile
 515 520 525
 Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr
 530 535 540
 Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe
 545 550 555 560
 Lys Cys Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly
 565 570 575

Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val
580 585 590
Val Ala Ser Leu Val Pro Ala Ala
595 600

<210> 37
<211> 1929
<212> DNA
<213> *Exophiala spinifera*

<220>
<221> intron
<222> (739)...(811)

<221> intron
<222> (1134)...(1186)

<400> 37
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cacatcgggc taggccc aaa cgaagcgagg tatgtgacaa tagctggaca gattggacaa 120
gacgcttttg gcgtagacaga cccagcctac gagaaacagg ttgcccagc attcgccaat 180
ctgcgagctt gccttgcgtgc agttggagcc tcttcaaacg acgtcaccaa gctcaattac 240
tacatcgtcg actacgcccc gagcaaactc accgcaattg gagatgggct gaagtctacc 300
tttgcccttg acaggctccc tccttgacag ctgggtgccag taccggcctt ggcttcacct 360
gaatacctct ttgaggttga cgccacggcg ctgggtgccag gacactcgac cccagacaaac 420
gttgccggacg tggtagtggt gggcgctggc ttgagcggtc tggagacggc acgcaaagtc 480
caggccgccc gtctgtcctg cctcgttctt gaggcgatgg atcgtgtagg gggaaagact 540
ctgagcgtag aatcgggtcc cggcaggacg actatcaacg acctcggcgc tgcgtggatc 600
aatgacagca accaaagcga agtatccaga ttgtttgaaa gatttcattt ggagggcgag 660
ctccagagga cgaccggaaa ttcaatccat caagcacaag acggtacaac cactacagct 720
ccttatgggtg actccccggg aagcacaatc ccactttgtg atgagacctc tgcgtgagtg 780
agaatacagt cactgactcc acttcgtcca gctgagcgag gaggttgcaa gtgcacttgc 840
ggaactcctc cccgtatggt ctcagctgat cgaagagtat agccttgaag accccaaggc 900
gagccctcag gcgaagcggc tcgacagtgt gagcttcgag cactactgtg agaaggacct 960
aaacttgctt gctgttctca gcgtggcaaa ccagatcaca cgcgctctgc tcggtgtgga 1020
agcccacgag atcagcatgc tttttctcac cgactacatc aagagtgcc aagggtctcag 1080
taatattgtc tcggacaaga aagacggcgg gcagtatatg cgatgcaaaa cagggtgcgtg 1140
cgggtgtctc tcaggtaggg gactcgtttc ttagtggtca ttccagggtat gcagtcgatt 1200
tgccatgcca tgtcaaagga acttgttcca ggctcagtg acctcaaac ccccgctcgt 1260
ggaattgagc agtcggcgtc cggctgtata gtacgatcgg cctcgggcgc cgtgttccga 1320
agcaaaaagg tgggtggttc gttaccgaca acattgtatc ccaccttgac attttcacca 1380
cctcttcccc cggagaagca agcattggcg gaaaaatcta tcctcggtca ctatagcaag 1440
atagtcttcg tatgggacaa cccgtgggtg cggaacaag gcttctcggt cgctctccaa 1500
tcgagctgtg accccatctc atttgccaga gataccagca tcgaagtcga tcggcaatgg 1560
tccattacct gtttcatggt cggagaccgc ggacggaagt ggtcccaaca gtccaagcag 1620
gtacgacaaa agtctgtctg ggaccaactc cgcgcagcct acgagaacgc cggggcccaa 1680
gtcccagagc cggccaacgt gctcgaaatc gagtggtcga agcagcagta tttccaagga 1740
gctccgagcg ccgtctatgg gctgaacgat ctcacacac tgggttcggc gctcagaacg 1800
ccgttcaagt gtgttcattt cgttgaacg gagacgtctt tagtttgga agggatatatg 1860
gaaggggcca tacgatcggg tcaacgaggt gctgcagaag ttgtggctag cctggtgcca 1920
gcagcatag 1929

<210> 38
<211> 600
<212> PRT
<213> *Exophiala spinifera*

<400> 38
Met Ala Leu Ala Pro Ser Tyr Ile Asn Pro Pro Asn Val Ala Ser Pro
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Ala Gly Tyr Ser His Ile Gly Val Gly Pro Asn Glu Ala Arg Tyr Val
20 25 30

Glu	Trp	Ser	Lys	Gln	Gln	Tyr	Phe	Gln	Gly	Ala	Pro	Ser	Ala	Val	Tyr
530						535					540				
Gly	Leu	Asn	Asp	Leu	Ile	Thr	Leu	Gly	Ser	Ala	Leu	Arg	Thr	Pro	Phe
545					550					555					560
Lys	Cys	Val	His	Phe	Val	Gly	Thr	Glu	Thr	Ser	Leu	Val	Trp	Lys	Gly
			565						570					575	
Tyr	Met	Glu	Gly	Ala	Ile	Arg	Ser	Gly	Gln	Arg	Gly	Ala	Ala	Glu	Val
			580					585					590		
Val	Ala	Ser	Leu	Val	Pro	Ala	Ala								
	595					600									

<210> 39
 <211> 1930
 <212> DNA
 <213> *Exophiala spinifera*

<220>
 <221> intron
 <222> (739)...(811)

<221> intron
 <222> (1134)...(1187)

<221> misc_feature
 <222> (648)...(648)
 <223> n = A,T,C or G

<400> 39

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cacgtcggcg	taggcccaga	cggagggagg	tatgtgacaa	tagctggaca	gattggacaa	120
gacgtctcgg	gcgtgacaga	cctgectac	gagaaacagg	ttgcccagc	attcgccaat	180
ctgcgagctt	gccttgctgc	agttggagcc	acttcaaacg	acgtcaccaa	gctcaattac	240
tacatcgtcg	actacgcccc	gagcaaactc	accgcaattg	gagatgggct	gaaggctacc	300
tttgcccttg	acaggctccc	tccttgacag	ctggtgccag	tgctggcctt	gtcttcacct	360
gaatacctct	ttgaggttga	tgccacggcg	ctggtgccgg	gacacacgac	cccagacaac	420
gttgcgggacg	tggtagtggg	gggcgctggc	ttgagcgggt	tggagacggc	acgcaaagtc	480
caggccgccc	gtctgtcctg	cctcgttctt	gaggcgatgg	atcgtgtagg	gggaaagact	540
ctgagcgtag	aatcggttcc	cggcaggacg	actatcaacg	acctcggcgc	tgctgggac	600
aatgacagca	accaaagcga	agtatccaga	ttgtttgaaa	gatttcatnt	ggagggcgag	660
ctccagagga	cgactggaaa	ttcaatccat	caagcacaag	acggtacaac	cactacagct	720
ccttatgggtg	actccttggg	aagcacaatc	ccactttgtg	atgagacctc	tgctcagtg	780
agaatacagt	cactgattcc	acttcgtcca	gctgagcgag	gaggttgcaa	gtgcacttgc	840
ggaaactcctc	cccgtatggg	ctcagctgat	cgaagagcat	agccttcaag	acctcaaggc	900
gagccctcag	gcgaagcggc	tcgacagtgt	gagcttcgcg	cactactgtg	agaaggaact	960
aaacttgcc	gctgttctcg	gcgtagcaaa	ccagatcaca	cgcgctctgc	tcggtgtgga	1020
agcccacgag	atcagcatgc	ttttctcac	cgactacatc	aagagtgcc	ccggtctcag	1080
taatattttc	tcggacaaga	aagacggcgg	gcagtatatg	cgatgcaaaa	caggtgcgtg	1140
tggtgtcgtc	tcaggtgggg	gactcgtttc	tcaagtgggtc	atttcaggta	tgacgtcgat	1200
ttgccatgcc	atgtcaaagg	aacttgttcc	aggctcagtg	cacctcaaca	ccccgctcgc	1260
tgaaattgag	cagtcggcat	ccggctgtac	agtacgatcg	gcctcggggc	ccgtgttccg	1320
aagcaaaaag	gtggtgggtt	cgttaccgac	aaccttgat	cccacctga	cattttcacc	1380
acctctcccc	gcccagaaagc	aagcattggc	ggaaaattct	atcctgggct	actatagcaa	1440
gatagtcttc	gtatgggaca	agccgtgggtg	gcgcgaacaa	ggcttctcgg	gcgtcctcca	1500
atcgagctgt	gaccccatct	catttgccag	agataccagc	atcgacgtcg	atcgacaatg	1560
gtccattacc	gttttcattg	tcggagaccc	gggacggaag	tggtcccaac	agtcacaagca	1620
ggtagcagaa	aagtctgtct	gggaccaact	ccgcgcagcc	tacgagaacg	ccggggccca	1680
agtcccagag	ccggccaacg	tgctcgaat	cgagtgggtcg	aagcagcagt	atttccaagg	1740
agctccgagc	gccgtctatg	ggctgaacga	tctcatcaca	ctgggttcgg	cgctcagaac	1800
gccgttcaag	agtgttcatt	tcgttgaac	ggagacgtct	ttagtttgga	aagggtatat	1860
ggaagggggc	atacgatcgg	gtcaacgagg	tgctgcagaa	gttgtggcta	gcctgggtgc	1920
agcagcatag						1930

<210> 40
 <211> 598
 <212> PRT
 <213> Exophiala spinifera

<220>
 <221> VARIANT
 <222> (216)...(216)
 <223> Xaa = Any Amino Acid

<400> 40
 Met Ala Leu Ala Pro Ser Tyr Ile Asn Pro Pro Asn Val Ala Ser Pro
 1 5 10 15
 Ala Gly Tyr Ser His Val Gly Val Gly Pro Asp Gly Gly Arg Tyr Val
 20 25 30
 Thr Ile Ala Gly Gln Ile Gly Gln Asp Ala Ser Gly Val Thr Asp Pro
 35 40 45
 Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys
 50 55 60
 Leu Ala Ala Val Gly Ala Thr Ser Asn Asp Val Thr Lys Leu Asn Tyr
 65 70 75 80
 Tyr Ile Val Asp Tyr Ala Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly
 85 90 95
 Leu Lys Ala Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val
 100 105 110
 Pro Val Ser Ala Leu Ser Ser Pro Glu Tyr Leu Phe Glu Val Asp Ala
 115 120 125
 Thr Ala Leu Val Pro Gly His Thr Thr Pro Asp Asn Val Ala Asp Val
 130 135 140
 Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln
 145 150 155 160
 Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly
 165 170 175
 Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile Asn
 180 185 190
 Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Ser
 195 200 205
 Arg Leu Phe Glu Arg Phe His Xaa Glu Gly Glu Leu Gln Arg Thr Thr
 210 215 220
 Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala Pro
 225 230 235 240
 Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu
 245 250 255
 Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln Asp
 260 265 270
 Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe Ala
 275 280 285
 His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val Asn
 290 295 300
 Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser Met
 305 310 315 320
 Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn Ile
 325 330 335
 Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr Gly
 340 345 350
 Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro Gly Ser
 355 360 365
 Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser Gly
 370 375 380
 Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys Lys Val
 385 390 395 400
 Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe Ser Pro

				405				410					415				
Pro	Leu	Pro	Ala	Glu	Lys	Gln	Ala	Leu	Ala	Glu	Asn	Ser	Ile	Leu	Gly		
			420					425					430				
Tyr	Tyr	Ser	Lys	Ile	Val	Phe	Val	Trp	Asp	Lys	Pro	Trp	Trp	Arg	Glu		
		435					440				445						
Gln	Gly	Phe	Ser	Gly	Val	Leu	Gln	Ser	Ser	Cys	Asp	Pro	Ile	Ser	Phe		
	450					455				460							
Ala	Arg	Asp	Thr	Ser	Ile	Asp	Val	Asp	Arg	Gln	Trp	Ser	Ile	Thr	Cys		
465					470					475					480		
Phe	Met	Val	Gly	Asp	Pro	Gly	Arg	Lys	Trp	Ser	Gln	Gln	Ser	Lys	Gln		
			485					490						495			
Val	Arg	Gln	Lys	Ser	Val	Trp	Asp	Gln	Leu	Arg	Ala	Ala	Tyr	Glu	Asn		
			500					505					510				
Ala	Gly	Ala	Gln	Val	Pro	Glu	Pro	Ala	Asn	Val	Leu	Glu	Ile	Glu	Trp		
		515					520					525					
Ser	Lys	Gln	Gln	Tyr	Phe	Gln	Gly	Ala	Pro	Ser	Ala	Val	Tyr	Gly	Leu		
	530					535				540							
Asn	Asp	Leu	Ile	Thr	Leu	Gly	Ser	Ala	Leu	Arg	Thr	Pro	Phe	Lys	Ser		
545					550					555					560		
Val	His	Phe	Val	Gly	Thr	Glu	Thr	Ser	Leu	Val	Trp	Lys	Gly	Tyr	Met		
			565					570						575			
Glu	Gly	Ala	Ile	Arg	Ser	Gly	Gln	Arg	Gly	Ala	Ala	Glu	Val	Val	Ala		
		580					585						590				
Ser	Leu	Val	Pro	Ala	Ala												
		595															

<210> 41
 <211> 1928
 <212> DNA
 <213> Rhinocycladiella atrovirens

<220>
 <221> intron
 <222> (739) ... (811)

 <221> intron
 <222> (1134) ... (1185)

<400> 41																	
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cacgtcggcg	taggcccaaa	cggagggagg	tatgcgacaa	tagctggaca	gattggacaa											120	
gacgcttcgg	ccgtgacaga	ccctgcctac	gagaaacagg	ttgcccaagc	attcgccaac											180	
ctgcgagctt	gtcttgctgc	agttggagcc	acttcaaacg	acattacca	gtcgaattac											240	
tacatcgtcg	actacaaccc	gagcaaactc	accgcaattg	gagatgggct	gaaggctacc											300	
tttgcccttg	acaggctccc	tccttgcaag	ctgggtgccg	tgccggccct	ggcttcacct											360	
gaataccccc	ttgaggttga	tgccacggcg	ctgggtccag	gacactcaac	cccagacaat											420	
gttgcgggac	tggtcgtggg	gggcgctggc	ttgagcgggt	tgagacggc	acgcaaagtc											480	
caggctgccc	ggctgtcctg	cctcgttctt	gaggcgatgg	atcgtgtggg	gggaaagact											540	
ctgagcgtac	aatcgggtcc	cggcaggacg	gctatcaatg	acctcggcgc	tgctgtggatc											600	
aatgacagca	accaaagcga	agtattcaaa	ttatttgaaa	gatttcattt	ggagggcgag											660	
ctccagagga	cgaccggaaa	ttcaatccat	caagcacaag	acggtacaac	cactacagct											720	
ccttatgggtg	attccctggg	aagcacaatt	ccatcttggtg	atgagacctc	tgctgtgtgt											780	
agaatacagt	cgctgactcc	acatcgtcca	gctgagcgag	gaggttgcaa	gtgcactcgc											840	
ggaactcctt	cccgcattgg	ctcagctgat	cgaagagcat	agtcttgaag	accccaaggc											900	
gagccctcaa	gcgaagcagc	tcgacagtgt	gagcttcgca	cactactgtg	agaaggatct											960	
aagcttgcc	gctgttctcg	gcgtggcaaa	ccagatcaca	cgcgctctgc	tcggtgtgga											1020	
agcccacgag	atcagcatgc	tttttctcac	cgactacatc	aagagtgcc	ccggtctcag											1080	
taatattgtc	tcggataaga	aagacgggtg	gcagtatatg	cgatgcaaaa	caggtgcgtg											1140	
tggtgttctc	tcagtgggag	actcgtttct	tagtggatcat	tccaggtatg	cagtcgcttt											1200	
gccatgccat	gtcaaaggaa	cttggtccag	gctcagtgc	cctcaacacc	cccgtcgccg											1260	
aaattgagca	gtcggcatcc	ggctgtacag	tacgatcggc	ctcgggcggc	gtgttccgaa											1320	
gtaaaaagg	ggtggtttcg	ttaccgacaa	ccttgatatc	caccttgata	ttttcaccac											1380	

ctcttcccgc	cgagaagcaa	gcattggctg	aaaaatccat	cctgggctac	tatagcaaga	1440
tagtcttcgt	atgggacaag	ccgtgggtggc	gcgaacaagg	cttctcgggc	gtcctccaat	1500
cgagctgtga	ccccatctca	tttgccagag	ataccagcat	cgaagtcgat	cggcaatggt	1560
ccattacctg	tttcatggtc	ggagaccggg	gacggaagt	gtcccaacag	tccaagcagg	1620
tacgacagaa	gtctgtctgg	aaccaactcc	gcccagccta	cgagaacgcc	ggggcccaag	1680
tcccagagcc	ggccaacgtg	ctcgagatcg	agtggtcgaa	gcagcagtat	ttccaaggag	1740
cgccgagcgt	cgtctatggg	ctgaactgtc	tcaacacact	gggttcggcg	ctcagaacgc	1800
cgttcaaggg	tgttcatttc	gttggaacgg	agacgtcttt	ggtttggaaa	gggtatatgg	1860
aaggggccat	acgatcgggt	cagcgaggcg	ctgcagaagt	tgtggctagc	ctggtgccag	1920
cagcatag						1928

<210> 42
 <211> 598
 <212> PRT
 <213> *Rhinocycladiella atrovirens*

<400> 42

Met	Ala	Leu	Ala	Pro	Ser	Tyr	Ile	Asn	Pro	Pro	Asn	Leu	Ala	Ser	Pro	1	5	10	15
Ala	Gly	Tyr	Ser	His	Val	Gly	Val	Gly	Pro	Asn	Gly	Gly	Arg	Tyr	Ala	20	25	30	
Thr	Ile	Ala	Gly	Gln	Ile	Gly	Gln	Asp	Ala	Ser	Ala	Val	Thr	Asp	Pro	35	40	45	
Ala	Tyr	Glu	Lys	Gln	Val	Ala	Gln	Ala	Phe	Ala	Asn	Leu	Arg	Ala	Cys	50	55	60	
Leu	Ala	Ala	Val	Gly	Ala	Thr	Ser	Asn	Asp	Ile	Thr	Lys	Leu	Asn	Tyr	65	70	75	80
Tyr	Ile	Val	Asp	Tyr	Asn	Pro	Ser	Lys	Leu	Thr	Ala	Ile	Gly	Asp	Gly	85	90	95	
Leu	Lys	Ala	Thr	Phe	Ala	Leu	Asp	Arg	Leu	Pro	Pro	Cys	Thr	Leu	Val	100	105	110	
Pro	Val	Pro	Ala	Leu	Ala	Ser	Pro	Glu	Tyr	Pro	Phe	Glu	Val	Asp	Ala	115	120	125	
Thr	Ala	Leu	Val	Pro	Gly	His	Ser	Thr	Pro	Asp	Asn	Val	Ala	Asp	Val	130	135	140	
Val	Val	Val	Gly	Ala	Gly	Leu	Ser	Gly	Leu	Glu	Thr	Ala	Arg	Lys	Val	145	150	155	160
Gln	Ala	Ala	Gly	Leu	Ser	Cys	Leu	Val	Leu	Glu	Ala	Met	Asp	Arg	Val	165	170	175	
Gly	Gly	Lys	Thr	Leu	Ser	Val	Gln	Ser	Gly	Pro	Gly	Arg	Thr	Ala	Ile	180	185	190	
Asn	Asp	Leu	Gly	Ala	Ala	Trp	Ile	Asn	Asp	Ser	Asn	Gln	Ser	Glu	Val	195	200	205	
Phe	Lys	Leu	Phe	Glu	Arg	Leu	Glu	Gly	Glu	Leu	Gln	Arg	Thr	Thr	Gly	210	215	220	
Asn	Ser	Ile	His	Gln	Ala	Gln	Asp	Gly	Thr	Thr	Thr	Thr	Ala	Pro	Tyr	225	230	235	240
Gly	Asp	Ser	Leu	Leu	Ser	Glu	Glu	Val	Ala	Ser	Ala	Leu	Ala	Glu	Leu	245	250	255	
Leu	Pro	Ala	Trp	Ser	Gln	Leu	Ile	Glu	Glu	His	Ser	Leu	Glu	Asp	Pro	260	265	270	
Lys	Ala	Ser	Pro	Gln	Ala	Lys	Gln	Leu	Asp	Ser	Val	Ser	Phe	Ala	His	275	280	285	
Tyr	Cys	Glu	Lys	Asp	Leu	Ser	Leu	Pro	Ala	Val	Leu	Gly	Val	Ala	Asn	290	295	300	
Gln	Ile	Thr	Arg	Ala	Leu	Leu	Gly	Val	Glu	Ala	His	Glu	Ile	Ser	Met	305	310	315	320
Leu	Phe	Leu	Thr	Asp	Tyr	Ile	Lys	Ser	Ala	Thr	Gly	Leu	Ser	Asn	Ile	325	330	335	
Val	Ser	Asp	Lys	Lys	Asp	Gly	Gly	Gln	Tyr	Met	Arg	Cys	Lys	Thr	Gly	340	345	350	
Met	Gln	Ser	Leu	Cys	His	Ala	Met	Ser	Lys	Glu	Leu	Val	Pro	Gly	Ser				

355	Val His Leu Asn Thr Pro	360	Val Ala Glu Ile Glu Gln Ser Ala Ser Gly	365	
370	Cys Thr Val Arg Ser Ala	375	Ser Gly Gly Val Phe Arg Ser Lys Lys Val	380	
385	Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Ile Phe Ser Pro	390		395	400
	405		410		415
Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Lys Ser Ile Leu Gly	420		425		430
Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp Arg Glu	435		440		445
Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser Phe	450		455		460
Ala Arg Asp Thr Ser Ile Glu Val Asp Arg Gln Trp Ser Ile Thr Cys	465		470		475
Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser Lys Gln	485		490		495
Val Arg Gln Lys Ser Val Trp Asn Gln Leu Arg Ala Ala Tyr Glu Asn	500		505		510
Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile Glu Trp	515		520		525
Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Val Val Tyr Gly Leu	530		535		540
Asn Cys Leu Asn Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys Gly	545		550		555
Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr Met	565		570		575
Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val Val Ala	580		585		590
Ser Leu Val Pro Ala Ala	595				

<210> 43
 <211> 1928
 <212> DNA
 <213> *Rhinocycladiella atrovirens*

<220>
 <221> intron
 <222> (739)...(811)

 <221> intron
 <222> (1134)...(1186)

<400> 43	
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tacgtcggcg taggccc aaa cggagggagg tatgtgacaa tagctggaca gattggacaa	120
gacgcttcgg ccgtgacaga cctgcctac gagaaacagg ttgccc aagc attcgccaac	180
ctgcgagctt gtcttgctgc agttggagcc acttcaa acg acattaccaa gctcaattac	240
tacatcgtcg actacaaccc gagcaaactc accgcaattg gagatgggct gaaggctacc	300
tttgcccttg acaggctccc tccttgcaag ctgggtgccag tgccggccct ggcttcacct	360
gaatacctct ttgaggttga tgccacggcg ctgggtccag gacactcaac cccagacaat	420
gttgcggacg tggctcgtggg gggcgctggc ttgagcgggt tggagacggc acgcaaagtc	480
caggctgccc ggctgtcctg cctcgtttct gagggcgatgg atcgtgtggg gggaaagact	540
ctgagcgtac aatcgggtcc cggcaggacg actatcaatg acctcggcgc tgcgtggatc	600
aatgacagca accaaagcga agtattcaaa ttatttgaaa gatttcattt ggagggcgag	660
ctccagagga cgaccggaaa ttcaatccat caagcacaag acggtacaac cactacagct	720
ccttatgggtg attccctggg aagcacaatt ccatcttggt atgagacctc tgtcgtgtgt	780
agaatacagt cgctgactcc acatcgtcca gctgagcag gaggttgcaa gtgcactcgc	840
ggaactcctt cccgcatggg ctcagctgat cgaagagcat agtcttgaag accccaaggc	900
gagccctcaa gcgaagcagc tcgacagtgt gagcttcgca cactactgtg agaaggatct	960
aaacttgcct gctgttctcg gcgtggcaaa ccagatcaca cgcgctctgc tcgggtgtgga	1020

agcccacgag	atcagcatgt	tttttctcac	cgactacatc	aagagtgcc	ccggtctcag	1080
taatatgtgc	tcggataaga	aagacggtgg	gcagtatatg	cgatgcaaaa	caggtgcgtg	1140
tggtgtttctc	tcagtgaggag	actcgtttct	tagtggtcat	tccaggtatg	cagtcgcttt	1200
gccatgccat	gtcaaaggaa	cttggtccag	gctcagtga	cctcaacacc	cccgtcgccg	1260
aaattgagca	gtcggcatcc	ggctgtacag	tacgatcggc	ctcgggcggc	gtgttccgaa	1320
gtaaaaagggt	ggtggtttcg	ttaccgacaa	ccttgatatcc	caccttgata	ttttcaccac	1380
ctcttcccg	cgagaagcaa	gcattggctg	aaaaatccat	cctggggtac	tatagcaaga	1440
tagtcttcgt	atgggacaag	ccgtgggtggc	gcgaacaagg	cttctcgggc	gtcctccaat	1500
cgagctgtga	ccccatctca	tttgccagag	ataccagcat	cgaagtcgat	cggcaatggt	1560
ccattacctg	tttcatggtc	ggagaccggg	gacggaagtg	gtcccaacag	tccaagcagg	1620
tacgacagaa	gtctgtctgg	aaccaactcc	gcgcagccta	cgagaacgcc	ggggcccaag	1680
tccagagacc	ggccaacgtg	ctcgagatcg	agtgggtcgaa	gcagcagtat	ttccaaggag	1740
cgccgagcgc	cgtctatggg	ctgaactgtc	tcaacacact	gggttcggcg	ctcagaacgc	1800
cgttcaagg	tggtcatttc	gttggaacgg	agacgtcttt	gggttggaag	gggtatatgg	1860
aaggggccat	acgatcgggt	cagcgaggcg	ctgcagaagt	tgtggctagc	ctgggtgccag	1920
cagcatag						1928

<210> 44
 <211> 591
 <212> PRT
 <213> *Rhinocycladiella atrovirens*

<400> 44															
Met	Ala	Leu	Ala	Pro	Ser	Tyr	Ile	Asn	Pro	Pro	Asn	Leu	Ala	Ser	Pro
1				5					10					15	
Ala	Gly	Tyr	Ser	Tyr	Val	Gly	Val	Gly	Pro	Asn	Gly	Gly	Arg	Tyr	Val
			20					25					30		
Thr	Ile	Ala	Gly	Gln	Ile	Gly	Gln	Asp	Ala	Ser	Ala	Val	Thr	Asp	Pro
		35					40					45			
Ala	Tyr	Glu	Lys	Gln	Val	Ala	Gln	Ala	Phe	Ala	Asn	Leu	Arg	Ala	Cys
	50					55					60				
Leu	Ala	Ala	Val	Gly	Ala	Thr	Ser	Asn	Asp	Ile	Thr	Lys	Leu	Asn	Tyr
65					70					75				80	
Tyr	Ile	Val	Asp	Tyr	Asn	Pro	Ser	Lys	Leu	Thr	Ala	Ile	Gly	Asp	Gly
			85					90						95	
Leu	Lys	Ala	Thr	Phe	Ala	Leu	Asp	Arg	Leu	Pro	Pro	Cys	Thr	Leu	Val
		100						105					110		
Pro	Val	Pro	Ala	Leu	Ala	Ser	Pro	Glu	Tyr	Leu	Phe	Glu	Val	Asp	Ala
		115					120					125			
Thr	Ala	Leu	Val	Pro	Gly	His	Ser	Thr	Pro	Asp	Asn	Val	Ala	Asp	Val
	130					135					140				
Val	Val	Val	Gly	Ala	Gly	Leu	Ser	Gly	Leu	Glu	Thr	Ala	Arg	Lys	Val
145					150					155					160
Gln	Ala	Ala	Gly	Leu	Ser	Cys	Leu	Val	Leu	Glu	Ala	Met	Asp	Arg	Val
			165					170					175		
Gly	Gly	Lys	Thr	Leu	Ser	Val	Gln	Ser	Gly	Gly	Arg	Thr	Thr	Ile	Asn
		180					185						190		
Asp	Leu	Gly	Ala	Ala	Trp	Ile	Asn	Asp	Ser	Asn	Gln	Ser	Glu	Val	Lys
	195						200					205			
Leu	Phe	Glu	Arg	Phe	His	Leu	Glu	Gly	Glu	Leu	Gln	Arg	Thr	Thr	Gly
	210					215					220				
Asn	Ser	Ile	His	Gln	Ala	Gln	Asp	Gly	Thr	Thr	Thr	Ala	Pro	Tyr	
225				230						235				240	
Gly	Ser	Leu	Leu	Ser	Glu	Glu	Val	Ala	Ser	Ala	Leu	Ala	Glu	Leu	Leu
			245					250					255		
Pro	Ala	Ser	Gln	Leu	Ile	Glu	Glu	His	Ser	Leu	Glu	Asp	Pro	Lys	Ala
		260					265					270			
Ser	Pro	Gln	Ala	Lys	Gln	Leu	Asp	Ser	Val	Ser	Phe	Ala	His	Tyr	Cys
	275						280					285			
Glu	Lys	Leu	Asn	Leu	Ala	Val	Leu	Gly	Val	Ala	Asn	Gln	Ile	Thr	Arg
	290					295					300				
Ala	Leu	Leu	Gly	Val	Glu	Ala	His	Glu	Ile	Ser	Met	Phe	Phe	Leu	Thr

305		310		315		320
Asp Tyr Ile Lys	Ser Ala Thr Gly Leu	Ser Asn Ile Val Ser	Asp Lys			
	325	330	335			
Lys Asp Gly Gly	Gln Tyr Met Arg Cys	Lys Thr Gly Met Gln	Ser Leu			
	340	345	350			
Cys His Ala Met	Ser Lys Glu Leu Val	Pro Gly Ser Val His	Leu Asn			
	355	360	365			
Thr Pro Val Ala	Glu Ile Glu Gln Ser Ala	Ser Gly Cys Thr Val	Arg			
	370	375	380			
Ser Ala Ser Gly	Gly Val Phe Arg Ser Lys	Lys Val Val Leu Pro	Thr			
	385	390	395			400
Leu Tyr Pro Thr	Leu Ile Phe Ser Pro Pro	Leu Pro Ala Glu Lys	Gln			
	405	410	415			
Ala Leu Ala Glu	Lys Ser Ile Leu Gly Tyr	Tyr Ser Lys Ile Val	Phe			
	420	425	430			
Val Trp Asp Lys	Pro Trp Trp Arg Glu Gln	Gly Phe Ser Gly Val	Leu			
	435	440	445			
Gln Ser Ser Cys	Asp Pro Ile Ser Phe Ala	Arg Asp Thr Ser Ile	Glu			
	450	455	460			
Val Asp Arg Gln	Trp Ser Ile Thr Cys Phe	Met Val Gly Asp Pro	Gly			
	465	470	475			480
Arg Lys Trp Ser	Gln Gln Ser Lys Gln Val	Arg Gln Lys Ser Val	Trp			
	485	490	495			
Asn Gln Leu Arg	Ala Ala Tyr Glu Asn Ala	Gly Ala Gln Val Pro	Glu			
	500	505	510			
Pro Ala Asn Val	Leu Glu Ile Glu Trp Ser	Lys Gln Gln Tyr Phe	Gln			
	515	520	525			
Gly Ala Pro Ser	Ala Val Tyr Gly Leu Asn	Cys Leu Asn Thr Leu	Gly			
	530	535	540			
Ser Ala Leu Arg	Thr Pro Phe Lys Gly Val	His Phe Val Gly Thr	Glu			
	545	550	555			560
Thr Ser Leu Val	Trp Lys Gly Tyr Met Glu	Gly Ala Ile Arg Ser	Gly			
	565	570	575			
Gln Arg Gly Ala	Glu Val Val Ala Ser Leu	Val Pro Ala Ala				
	580	585	590			

<210> 45
 <211> 1928
 <212> DNA
 <213> Rhinocycladiella atrovirens

<220>
 <221> intron
 <222> (739)...(811)

 <221> intron
 <222> (1134)...(1185)

<400> 45							
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cacgtcggcg	taggcccacaa	cggagggagg	tatgtgacaa	tagctggaca	gattggacaa		120
gacgcttcgg	ccgtgacaga	ccctgectac	gagaaacagg	ttgcccagc	attcgccaac		180
ctgcgagctt	gtcttgctgc	agttggagcc	acttcaaacg	acattaccac	gctcaattac		240
tacatcgctg	actacaaccc	gagcaaactc	accgcaattg	gagatgggct	gaaggctacc		300
tttgcccttg	acaggctccc	tccttgcaag	ctgggtgccag	tgccggccct	ggcttcacct		360
gaatacctct	ttgaggttga	tgctacggcg	ctgggtccag	gacactcaac	cccagacaat		420
gttgcggacg	tggtcgtggt	gggcgctggc	ttgagcgggt	tggagacggc	acgcaaagtc		480
caggctgccg	ggctgtcctg	cctcgctctt	gaggcgatgg	atcgtgtggg	gggaaagact		540
ctgagcgtag	aatcgggtcc	cggcaggacg	actatcaatg	acctcggcgc	tgctgtggatc		600
aatgacagca	accaaagcga	agtattcaaa	ttatttgaaa	gatttcattt	ggagggcgag		660
ctccagagga	cgaccggaaa	ttcaatccat	caagcacaag	acggtacaac	cactacagct		720
ccttatggtg	attccctggt	aggcacaatt	ccatcttgtg	atgagacctc	tgctgtgtgt		780

agaatacagt	cgctgactcc	acatcgctcca	gctgagcgag	gaggttgcaa	gtgcactcgc	840
ggaactcctt	cccgcgatgt	ctcagctgat	cgaagagcat	agtcttgaag	accccaaggc	900
gagccctcaa	gcgaagcagc	tcgacagtgt	gagcttcgca	cactactgtg	agaaggatct	960
aaacttgctt	gctgtttctg	gcgtggcaaa	ccagatcaca	cgcgctctgc	tcggtgtgga	1020
agcccacgag	atcagcatgc	tttttctcac	cgactacatc	aagagtgcca	ccggtctcag	1080
taatattgtc	tcggataaga	aagacggtgg	gcagtatatg	cgatgcaaaa	caggtgcgtg	1140
tggtgtttct	tcagtgggag	actcgtttct	tagtggtcat	tccagggtatg	cagtcgcttt	1200
gccatgccat	gtcaaaggaa	cttggtccag	gctcagtga	cctcaacacc	cccgtcgccg	1260
aaattgagca	gtcggcatcc	ggctgtacag	tacgatcggc	ctcgggcggc	gtgttccgaa	1320
gtaaaaagg	ggtggtttcg	ttaccgacaa	ccttgatcc	caccttgata	ttttcaccac	1380
ctcttccgc	cgagaagcaa	gcattggctg	aaaaatccat	cctgggctac	tatagcaaga	1440
tagtcttcgt	atgggacaag	ctgtggtggc	gcgaacaagg	cttctcgggc	gtcctccaat	1500
cgagctgtga	ccccatctca	tttgccagag	ataccagcat	cgaagtcgat	cggcaatggt	1560
ccattacctg	tttcatggtc	ggagaccg	gacggaagt	gtcccaacag	tccaagcagg	1620
tacgacagaa	gtctgtctgg	aaccaactcc	gcgcagccta	cgagaacgcc	ggggcccaag	1680
tcccagagcc	ggccaacgtg	ctcgagatcg	agtggtcgaa	gcagcagtat	ttccaaggag	1740
cgcgcagcgc	cgtctatggg	ctgaactgtc	tcaacacact	gggttcggcg	ctcagaacgc	1800
cgttcaagg	tgttcatctt	gttggaaagg	agacgtcttt	ggtttggaag	gggtatatgg	1860
aaggggcat	acgatcgggt	cagcgaggcg	ctgcagaagt	tgtgcctagc	ctggtgccag	1920
cagcatag						1928

<210> 46

<211> 591

<212> PRT

<213> Rhinocycladiella atrovirens

<400> 46

Met	Ala	Leu	Ala	Pro	Ser	Tyr	Ile	Asn	Pro	Pro	Asn	Ala	Ser	Pro	Ala
1				5					10					15	
Gly	Tyr	Ser	His	Val	Gly	Val	Gly	Pro	Asn	Gly	Gly	Arg	Tyr	Val	Thr
			20					25					30		
Ile	Ala	Gly	Gln	Ile	Gly	Gln	Asp	Ala	Ser	Ala	Val	Thr	Asp	Pro	Ala
		35					40					45			
Tyr	Glu	Lys	Gln	Val	Ala	Gln	Ala	Phe	Ala	Asn	Leu	Arg	Ala	Cys	Leu
	50					55					60				
Ala	Ala	Val	Gly	Ala	Thr	Ser	Asn	Asp	Ile	Thr	Lys	Leu	Asn	Tyr	Tyr
65					70					75					80
Ile	Val	Asp	Tyr	Asn	Pro	Ser	Lys	Leu	Thr	Ala	Ile	Gly	Asp	Gly	Leu
				85					90					95	
Lys	Ala	Thr	Phe	Ala	Leu	Asp	Arg	Leu	Pro	Pro	Cys	Thr	Leu	Val	Pro
			100					105					110		
Val	Pro	Ala	Leu	Ala	Ser	Pro	Glu	Tyr	Leu	Phe	Glu	Val	Asp	Ala	Thr
	115						120					125			
Ala	Leu	Val	Pro	Gly	His	Ser	Thr	Pro	Asp	Asn	Val	Ala	Asp	Val	Val
	130					135					140				
Val	Val	Gly	Ala	Gly	Leu	Ser	Gly	Leu	Glu	Thr	Ala	Arg	Lys	Val	Gln
145					150					155					160
Ala	Ala	Gly	Leu	Ser	Cys	Leu	Val	Leu	Glu	Ala	Met	Asp	Arg	Val	Gly
			165					170						175	
Gly	Lys	Thr	Leu	Ser	Val	Gln	Ser	Gly	Pro	Gly	Arg	Thr	Thr	Ile	Asn
		180						185					190		
Asp	Leu	Gly	Ala	Ala	Trp	Ile	Asn	Asp	Ser	Asn	Gln	Ser	Glu	Val	Phe
	195					200					205				
Lys	Leu	Phe	Glu	Arg	Phe	His	Leu	Glu	Gly	Glu	Leu	Gln	Arg	Thr	Thr
	210					215					220				
Gly	Asn	Ser	Ile	His	Gln	Ala	Gln	Asp	Gly	Thr	Thr	Thr	Thr	Ala	Pro
225					230					235					240
Tyr	Gly	Asp	Ser	Leu	Leu	Ser	Glu	Glu	Val	Ala	Ser	Ala	Leu	Ala	Glu
			245						250					255	
Leu	Leu	Pro	Ala	Trp	Ser	Gln	Leu	Ile	Glu	Glu	His	Ser	Leu	Glu	Asp
		260						265					270		
Pro	Lys	Ala	Ser	Pro	Gln	Ala	Lys	Gln	Leu	Asp	Ser	Val	Ser	Phe	Ala

275	280	285
His Tyr Cys Glu Lys Asp Leu Asn Leu Pro Ala Val Leu Gly Val Ala		
290	295	300
Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser		
305	310	315
Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn		
325	330	335
Ile Val Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr		
340	345	350
Gly Met Gln Ser Leu Cys His Ala Met Ser Lys Glu Leu Val Pro Gly		
355	360	365
Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser		
370	375	380
Gly Cys Thr Val Arg Ser Ala Ser Gly Gly Val Phe Arg Ser Lys Lys		
385	390	395
Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Ile Phe Ser Pro Leu		
405	410	415
Pro Ala Glu Lys Gln Ala Leu Ala Glu Lys Ser Ile Gly Tyr Tyr Ser		
420	425	430
Lys Ile Val Phe Val Asp Lys Leu Trp Trp Arg Glu Gln Gly Phe Ser		
435	440	445
Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr		
450	455	460
Ser Ile Glu Val Asp Arg Gln Ser Ile Thr Cys Phe Met Val Gly Asp		
465	470	475
Pro Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val		
485	490	495
Trp Asn Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro		
500	505	510
Glu Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe		
515	520	525
Gln Ala Pro Ser Ala Val Tyr Gly Leu Asn Cys Leu Asn Thr Leu Gly		
530	535	540
Ser Ala Leu Arg Thr Pro Phe Lys Gly Val His Phe Val Gly Thr Glu		
545	550	555
Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly		
565	570	575
Gln Arg Gly Ala Ala Glu Val Val Pro Ser Leu Val Pro Ala Ala		
580	585	590

<210> 47
 <211> 600
 <212> PRT
 <213> Exophiala spinifera

<400> 47
Met Ala Leu Ala Pro Ser Tyr Ile Asn Pro Pro Asn Val Ala Ser Pro
1 5 10 15
Ala Gly Tyr Ser His Val Gly Val Gly Pro Asp Gly Gly Arg Tyr Val
20 25 30
Thr Ile Ala Gly Gln Ile Gly Gln Asp Ala Ser Gly Val Thr Asp Pro
35 40 45
Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys
50 55 60
Leu Ala Ala Val Gly Ala Thr Ser Asn Asp Val Thr Lys Leu Asn Tyr
65 70 75 80
Tyr Ile Val Asp Tyr Ala Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly
85 90 95
Leu Lys Ala Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val
100 105 110
Pro Val Ser Ala Leu Ser Ser Pro Glu Tyr Leu Phe Glu Val Asp Ala
115 120 125

Thr	Ala	Leu	Val	Pro	Gly	His	Thr	Thr	Pro	Asp	Asn	Val	Ala	Asp	Val	130	135	140
Val	Val	Val	Gly	Ala	Gly	Leu	Ser	Gly	Leu	Glu	Thr	Ala	Arg	Lys	Val	145	150	155
Gln	Ala	Ala	Gly	Leu	Ser	Cys	Leu	Val	Leu	Glu	Ala	Met	Asp	Arg	Val	165	170	175
Gly	Gly	Lys	Thr	Leu	Ser	Val	Gln	Ser	Gly	Pro	Gly	Arg	Thr	Thr	Ile	180	185	190
Asn	Asp	Leu	Gly	Ala	Ala	Trp	Ile	Asn	Asp	Ser	Asn	Gln	Ser	Glu	Val	195	200	205
Ser	Arg	Leu	Phe	Glu	Arg	Phe	His	Leu	Glu	Gly	Glu	Leu	Gln	Arg	Thr	210	215	220
Thr	Gly	Asn	Ser	Ile	His	Gln	Ala	Gln	Asp	Gly	Thr	Thr	Thr	Thr	Ala	225	230	235
Pro	Tyr	Gly	Asp	Ser	Leu	Leu	Ser	Glu	Glu	Val	Ala	Ser	Ala	Leu	Ala	245	250	255
Glu	Leu	Leu	Pro	Val	Trp	Ser	Gln	Leu	Ile	Glu	Glu	His	Ser	Leu	Gln	260	265	270
Asp	Leu	Lys	Ala	Ser	Pro	Gln	Ala	Lys	Arg	Leu	Asp	Ser	Val	Ser	Phe	275	280	285
Ala	His	Tyr	Cys	Glu	Lys	Glu	Leu	Asn	Leu	Pro	Ala	Val	Leu	Gly	Val	290	295	300
Ala	Asn	Gln	Ile	Thr	Arg	Ala	Leu	Leu	Gly	Val	Glu	Ala	His	Glu	Ile	305	310	315
Ser	Met	Leu	Phe	Leu	Thr	Asp	Tyr	Ile	Lys	Ser	Ala	Thr	Gly	Leu	Ser	325	330	335
Asn	Ile	Phe	Ser	Asp	Lys	Lys	Asp	Gly	Gly	Gln	Tyr	Met	Arg	Cys	Lys	340	345	350
Thr	Gly	Met	Gln	Ser	Ile	Cys	His	Ala	Met	Ser	Lys	Glu	Leu	Val	Pro	355	360	365
Gly	Ser	Val	His	Leu	Asn	Thr	Pro	Val	Ala	Glu	Ile	Glu	Gln	Ser	Ala	370	375	380
Ser	Gly	Cys	Thr	Val	Arg	Ser	Ala	Ser	Gly	Ala	Val	Phe	Arg	Ser	Lys	385	390	395
Lys	Val	Val	Val	Ser	Leu	Pro	Thr	Thr	Leu	Tyr	Pro	Thr	Leu	Thr	Phe	405	410	415
Ser	Pro	Pro	Leu	Pro	Ala	Glu	Lys	Gln	Ala	Leu	Ala	Glu	Asn	Ser	Ile	420	425	430
Leu	Gly	Tyr	Tyr	Ser	Lys	Ile	Val	Phe	Val	Trp	Asp	Lys	Pro	Trp	Trp	435	440	445
Arg	Glu	Gln	Gly	Phe	Ser	Gly	Val	Leu	Gln	Ser	Ser	Cys	Asp	Pro	Ile	450	455	460
Ser	Phe	Ala	Arg	Asp	Thr	Ser	Ile	Asp	Val	Asp	Arg	Gln	Trp	Ser	Ile	465	470	475
Thr	Cys	Phe	Met	Val	Gly	Asp	Pro	Gly	Arg	Lys	Trp	Ser	Gln	Gln	Ser	485	490	495
Lys	Gln	Val	Arg	Gln	Lys	Ser	Val	Trp	Asp	Gln	Leu	Arg	Ala	Ala	Tyr	500	505	510
Glu	Asn	Ala	Gly	Ala	Gln	Val	Pro	Glu	Pro	Ala	Asn	Val	Leu	Glu	Ile	515	520	525
Glu	Trp	Ser	Lys	Gln	Gln	Tyr	Phe	Gln	Gly	Ala	Pro	Ser	Ala	Val	Tyr	530	535	540
Gly	Leu	Asn	Asp	Leu	Ile	Thr	Leu	Gly	Ser	Ala	Leu	Arg	Thr	Pro	Phe	545	550	555
Lys	Ser	Val	His	Phe	Val	Gly	Thr	Glu	Thr	Ser	Leu	Val	Trp	Lys	Gly	565	570	575
Tyr	Met	Glu	Gly	Ala	Ile	Arg	Ser	Gly	Gln	Arg	Gly	Ala	Ala	Glu	Val	580	585	590
Val	Ala	Ser	Leu	Val	Pro	Ala	Ala									595	600	

<211> 1392
 <212> DNA
 <213> Unknown

<220>
 <221> CDS
 <222> (1)...(1392)

<223> Cys (-) APAO; removal of cysteine 461

<400> 48
 aaa gac aac gtt gcg gac gtg gta gtg gtg ggc gct ggc ttg agc ggt 48
 Lys Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly
 1 5 10 15

ttg gag acg gca cgc aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt 96
 Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val
 20 25 30

ctt gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tcg 144
 Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser
 35 40 45

ggt ccc ggc agg acg act atc aac gac ctc ggc gct gcg tgg atc aat 192
 Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn
 50 55 60

gac agc aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg 240
 Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu
 65 70 75 80

gag ggc gag ctc cag agg acg act gga aat tca atc cat caa gca caa 288
 Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln
 85 90 95

gac ggt aca acc act aca gct cct tat ggt gac tcc ttg ctg agc gag 336
 Asp Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu
 100 105 110

gag gtt gca agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg 384
 Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu
 115 120 125

atc gaa gag cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag 432
 Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys
 130 135 140

cgg ctc gac agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac 480
 Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn
 145 150 155 160

ttg cct gct gtt ctc ggc gta gca aac cag atc aca cgc gct ctg ctc 528
 Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu
 165 170 175

ggt gtg gaa gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc 576
 Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile
 180 185 190

aag agt gcc acc ggt ctc agt aat att ttc tcg gac aag aaa gac ggc 624
 Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly
 195 200 205

ggg cag tat atg cga tgc aaa aca ggt atg cag tcg att tgc cat gcc	672
Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala	
210 215 220	
atg tca aag gaa ctt gtt cca ggc tca gtg cac ctc aac acc ccc gtc	720
Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val	
225 230 235 240	
gct gaa att gag cag tcg gca tcc ggc tgt aca gta cga tcg gcc tcg	768
Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser	
245 250 255	
ggc gcc gtg ttc cga agc aaa aag gtg gtg gtt tcg tta ccg aca acc	816
Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr	
260 265 270	
ttg tat ccc acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa	864
Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln	
275 280 285	
gca ttg gcg gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc	912
Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe	
290 295 300	
gta tgg gac aag ccg tgg tgg cgc gaa caa ggc ttc tcg ggc gtc ctc	960
Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu	
305 310 315 320	
caa tcg agc tcc gac ccc atc tca ttt gcc aga gat acc agc atc gac	1008
Gln Ser Ser Ser Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp	
325 330 335	
gtc gat cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga	1056
Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly	
340 345 350	
cgg aag tgg tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg	1104
Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp	
355 360 365	
gac caa ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag	1152
Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu	
370 375 380	
ccg gcc aac gtg ctc gaa atc gag tgg tcg aag cag cag tat ttc caa	1200
Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln	
385 390 395 400	
gga gct ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt	1248
Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly	
405 410 415	
tcg gcg ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag	1296
Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu	
420 425 430	
acg tct tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tcg ggt	1344
Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly	
435 440 445	
caa cga ggt gct gca gaa gtt gtg gct agc ctg gtg cca gca gca tag	1392

Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala *
 450 455 460

<210> 49
 <211> 463
 <212> PRT
 <213> Unknown

<220>
 <223> Cys (-) APAO; removal of cysteine 461

<400> 49
 Lys Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly
 1 5 10 15
 Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val
 20 25 30
 Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser
 35 40 45
 Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn
 50 55 60
 Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu
 65 70 75 80
 Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln
 85 90 95
 Asp Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu
 100 105 110
 Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu
 115 120 125
 Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys
 130 135 140
 Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn
 145 150 155 160
 Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu
 165 170 175
 Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile
 180 185 190
 Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly
 195 200 205
 Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala
 210 215 220
 Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val
 225 230 235 240
 Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser
 245 250 255
 Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr
 260 265 270
 Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln
 275 280 285
 Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe
 290 295 300
 Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu
 305 310 315 320
 Gln Ser Ser Ser Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp
 325 330 335
 Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly
 340 345 350
 Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp
 355 360 365
 Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu
 370 375 380
 Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln

ttg cct gct gtt ctc ggc gta gca aac cag atc aca cgc gct ctg ctc	528
Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu	
165 170 175	
ggg ggt gtg gaa gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc	576
Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile	
180 185 190	
aag agt gcc acc ggt ctc agt aat att ttc tcg gac aag aaa gac ggc	624
Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly	
195 200 205	
ggg cag tat atg cga tgc aaa aca ggt atg cag tcg att tcg cat gcc	672
Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Ser His Ala	
210 215 220	
atg tca aag gaa ctt gtt cca ggc tca gtg cac ctc aac acc ccc gtc	720
Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val	
225 230 235 240	
gct gaa att gag cag tcg gca tcc ggc tgt aca gta cga tcg gcc tcg	768
Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser	
245 250 255	
ggc gcc gtg ttc cga agc aaa aag gtg gtg gtt tcg tta ccg aca acc	816
Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr	
260 265 270	
ttg tat ccc acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa	864
Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln	
275 280 285	
gca ttg gcg gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc	912
Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe	
290 295 300	
gta tgg gac aag ccg tgg tgg cgc gaa caa ggc ttc tcg ggc gtc ctc	960
Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu	
305 310 315 320	
caa tcg agc tcc gac ccc atc tca ttt gcc aga gat acc agc atc gac	1008
Gln Ser Ser Ser Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp	
325 330 335	
gtc gat cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga	1056
Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly	
340 345 350	
cgg aag tgg tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg	1104
Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp	
355 360 365	
gac caa ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag	1152
Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu	
370 375 380	
ccg gcc aac gtg ctc gaa atc gag tgg tcg aag cag cag tat ttc caa	1200
Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln	
385 390 395 400	
gga gct ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt	1248
Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly	

405	410	415	
tcg gcg ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag			1296
Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu			
420	425	430	
acg tct tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tcg ggt			1344
Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly			
435	440	445	
caa cga ggt gct gca gaa gtt gtg gct agc ctg gtg cca gca gca tag			1392
Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala *			
450	455	460	

<210> 51
 <211> 463
 <212> PRT
 <213> Unknown

<220>
 <223> Cys (-) APAO; removal of cysteines 359 and 461

<400> 51

Lys	Asp	Asn	Val	Ala	Asp	Val	Val	Val	Val	Gly	Ala	Gly	Leu	Ser	Gly
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Leu	Glu	Thr	Ala	Arg	Lys	Val	Gln	Ala	Ala	Gly	Leu	Ser	Cys	Leu	Val
			20					25					30		
Leu	Glu	Ala	Met	Asp	Arg	Val	Gly	Gly	Lys	Thr	Leu	Ser	Val	Gln	Ser
		35					40					45			
Gly	Pro	Gly	Arg	Thr	Thr	Ile	Asn	Asp	Leu	Gly	Ala	Ala	Trp	Ile	Asn
50						55					60				
Asp	Ser	Asn	Gln	Ser	Glu	Val	Ser	Arg	Leu	Phe	Glu	Arg	Phe	His	Leu
65					70					75					80
Glu	Gly	Glu	Leu	Gln	Arg	Thr	Thr	Gly	Asn	Ser	Ile	His	Gln	Ala	Gln
				85					90					95	
Asp	Gly	Thr	Thr	Thr	Ala	Pro	Tyr	Gly	Asp	Ser	Leu	Leu	Ser	Glu	
			100					105					110		
Glu	Val	Ala	Ser	Ala	Leu	Ala	Glu	Leu	Leu	Pro	Val	Trp	Ser	Gln	Leu
		115					120					125			
Ile	Glu	Glu	His	Ser	Leu	Gln	Asp	Leu	Lys	Ala	Ser	Pro	Gln	Ala	Lys
130						135					140				
Arg	Leu	Asp	Ser	Val	Ser	Phe	Ala	His	Tyr	Cys	Glu	Lys	Glu	Leu	Asn
145					150					155					160
Leu	Pro	Ala	Val	Leu	Gly	Val	Ala	Asn	Gln	Ile	Thr	Arg	Ala	Leu	Leu
			165						170					175	
Gly	Val	Glu	Ala	His	Glu	Ile	Ser	Met	Leu	Phe	Leu	Thr	Asp	Tyr	Ile
			180					185					190		
Lys	Ser	Ala	Thr	Gly	Leu	Ser	Asn	Ile	Phe	Ser	Asp	Lys	Lys	Asp	Gly
			195				200					205			
Gly	Gln	Tyr	Met	Arg	Cys	Lys	Thr	Gly	Met	Gln	Ser	Ile	Ser	His	Ala
210						215					220				
Met	Ser	Lys	Glu	Leu	Val	Pro	Gly	Ser	Val	His	Leu	Asn	Thr	Pro	Val
225					230						235				240
Ala	Glu	Ile	Glu	Gln	Ser	Ala	Ser	Gly	Cys	Thr	Val	Arg	Ser	Ala	Ser
				245					250					255	
Gly	Ala	Val	Phe	Arg	Ser	Lys	Lys	Val	Val	Val	Ser	Leu	Pro	Thr	Thr
			260					265					270		
Leu	Tyr	Pro	Thr	Leu	Thr	Phe	Ser	Pro	Pro	Leu	Pro	Ala	Glu	Lys	Gln
		275					280					285			
Ala	Leu	Ala	Glu	Asn	Ser	Ile	Leu	Gly	Tyr	Tyr	Ser	Lys	Ile	Val	Phe
290						295						300			

Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu
 305 310 315 320
 Gln Ser Ser Ser Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp
 325 330 335
 Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly
 340 345 350
 Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp
 355 360 365
 Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu
 370 375 380
 Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln
 385 390 395 400
 Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly
 405 410 415
 Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu
 420 425 430
 Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly
 435 440 445
 Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala
 450 455 460

<210> 52
 <211> 1392
 <212> DNA
 <213> Unknown

<220>
 <221> CDS
 <222> (1)...(1392)

<223> Cys (-) APAO; removal of cysteines 169, 359, and
 461

<400> 52
 aaa gac aac gtt gcg gac gtg gta gtg gtg ggc gct ggc ttg agc ggt 48
 Lys Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly
 1 5 10 15
 ttg gag acg gca cgc aaa gtc cag gcc gcc ggt ctg agc tcc ctc gtt 96
 Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Ser Leu Val
 20 25 30
 ctt gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tcg 144
 Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser
 35 40 45
 ggt ccc ggc agg acg act atc aac gac ctc ggc gct gcg tgg atc aat 192
 Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn
 50 55 60
 gac agc aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg 240
 Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu
 65 70 75 80
 gag ggc gag ctc cag agg acg act gga aat tca atc cat caa gca caa 288
 Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln
 85 90 95
 gac ggt aca acc act aca gct cct tat ggt gac tcc ttg ctg agc gag 336
 Asp Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu
 100 105 110

gag gtt gca agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg	384
Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu	
115 120 125	
atc gaa gag cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag	432
Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys	
130 135 140	
cgg ctc gac agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac	480
Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn	
145 150 155 160	
ttg cct gct gtt ctc ggc gta gca aac cag atc aca cgc gct ctg ctc	528
Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu	
165 170 175	
ggt gtg gaa gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc	576
Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile	
180 185 190	
aag agt gcc acc ggt ctc agt aat att ttc tcg gac aag aaa gac ggc	624
Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly	
195 200 205	
ggg cag tat atg cga tgc aaa aca ggt atg cag tcg att tcg cat gcc	672
Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Ser His Ala	
210 215 220	
atg tca aag gaa ctt gtt cca ggc tca gtg cac ctc aac acc ccc gtc	720
Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val	
225 230 235 240	
gct gaa att gag cag tcg gca tcc ggc tgt aca gta cga tcg gcc tcg	768
Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser	
245 250 255	
ggc gcc gtg ttc cga agc aaa aag gtg gtg gtt tcg tta ccg aca acc	816
Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr	
260 265 270	
ttg tat ccc acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa	864
Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln	
275 280 285	
gca ttg gcg gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc	912
Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe	
290 295 300	
gta tgg gac aag ccg tgg tgg cgc gaa caa ggc ttc tcg ggc gtc ctc	960
Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu	
305 310 315 320	
caa tcg agc tcc gac ccc atc tca ttt gcc aga gat acc agc atc gac	1008
Gln Ser Ser Ser Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp	
325 330 335	
gtc gat cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga	1056
Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly	
340 345 350	
cgg aag tgg tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg	1104
Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp	

355	360	365	
gac caa ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag			1152
Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu			
370	375	380	
ccg gcc aac gtg ctc gaa atc gag tgg tcg aag cag cag tat ttc caa			1200
Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln			
385	390	395	400
gga gct ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt			1248
Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly			
405	410	415	
tcg gcg ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag			1296
Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu			
420	425	430	
acg tct tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tcg ggt			1344
Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly			
435	440	445	
caa cga ggt gct gca gaa gtt gtg gct agc ctg gtg cca gca gca tag			1392
Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala *			
450	455	460	

<210> 53
 <211> 463
 <212> PRT
 <213> Unknown

<220>
 <223> Cys (-) APAO; removal of cysteines 169, 359, and
 461

<400> 53
 Lys Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly
 1 5 10 15
 Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Ser Leu Val
 20 25 30
 Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser
 35 40 45
 Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn
 50 55 60
 Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu
 65 70 75 80
 Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln
 85 90 95
 Asp Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu
 100 105 110
 Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu
 115 120 125
 Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys
 130 135 140
 Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn
 145 150 155 160
 Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu
 165 170 175
 Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile
 180 185 190
 Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly

